

SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB#

49160

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____ NA Sequence (#) _____ STN _____
 Searcher Phone #: _____ AA Sequence (#) 1+1 Dialog Reverse font
 Searcher Location: _____ Structure (#) _____ Questel/Orbit: _____
 Date Searcher Picked Up: 8/17/01 Bibliographic _____ Dr. Link _____
 Date Completed: 8/19/01 Litigation _____ Lexis/Nexis _____
 Searcher Prep & Review Time: _____ Fulltext _____ Sequence Systems 01
 Clerical Prep Time: _____ Patent Family _____ WWW/Internet _____
 Online Time: _____ Other _____ Other (specify) _____

OM of: US-09-457-066-2_COPY_210_345 to: EST:* out_format : pfs

Date: Aug 18, 2001 4:10 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODE=framer_p2n.model -DEV=xlip
-q=/cgn2.1/USPTO_spool/US09457066/runat_17082001_083144_25044/app-query.fasta_1.207
-DB=EST -QFMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000
-MINWATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -XGAPOP=6.000
-OGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi
-LIST=45 -DALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USPR=US09457066 @CGN1_1.2722 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-457-066-2_COPY_210_345

Query length: 136

Database: EST:*

Database sequences: 10228115

Database length: 431459454

Search time (sec): 1369.120000

score_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
gb_est102:BG609411	+	708.00	1373.56	556	..
gb_est81:BE958470	+	705.00	1368.32	523	! BG609411 323251 MARC LPIG Sus s
gb_est82:BF021679	+	697.00	1352.66	523	! BE958470 601644787F1 NIH.MGC.58
gb_est83:BF151355	+	663.00	1285.31	564	! BF021679 uv50f05.y1 NCI.CGAP.Lu
gb_est84:BF102859	+	663.00	1285.31	564	! BF151355 ua15b12.y1 NCI.CGAP.Ma
gb_est85:BF102859	+	622.00	1200.76	851	! BF102859 601646827F1 NIH.MGC.60
gb_est86:BF0243001	+	606.00	1168.73	910	! BG243001 602355974F1 NCI.CGAP.M
gb_est87:BF011835	+	587.00	1138.92	447	! BF011835 us37d10.y1 Soares.NHEB
gb_est88:AL047637	+	568.00	1105.72	304	! AL047637 DKFZP58630421.r1 586.0
gb_est89:BF070092	+	538.50	1036.96	874	! BF070092 602119417F1 NIH.MGC.58
gb_est90:BF031624	+	523.00	1005.78	950	! BF031624 601558104F1 NIH.MGC.58
gb_est91:BF031624	+	507.00	974.26	968	! BG118707 602348280F1 NIH.MGC.90
gb_est92:BF031624	+	439.50	843.12	877	! AL180978 Tetraodon nigroviridis
gb_gss3:CN5024MX	-	381.00	728.29	902	! BF163629 601769732F1 NCI.CGAP.I
gb_hic:AK003359	+	345.50	651.63	1796	! AK003359 Mus musculus 18 days
gb_est15:AI020581	+	327.00	633.20	324	! AI020581 ua96c08.r1 Soares.mamm
gb_est73:BE374398	+	323.50	621.41	521	! BE374398 601227568F1 NCI.CGAP.M
gb_est44:AW210331	+	283.00	542.32	511	! AW210331 ui53f09.y1 Rashbass mc
gb_est11:AA759138	-	254.00	487.45	425	! AA759138 ah78f03.s1 Soares_test
gb_est20:AI470494	-	246.00	473.69	354	! AI470494 t144e11.x1 Soares.NSF
gb_est97:BG173847	+	228.50	428.34	1029	! BG173847 602333906F1 NCI.CGAP.L
gb_gss4:CN50458A	-	217.50	406.73	1036	! AL304867 Tetraodon nigroviridis
gb_est53:AW689905	+	215.50	409.21	560	! AW689905 ESTR30981 MAGE resequ
gb_est83:BF171726	+	214.00	421.77	126	! BF171726 uz07a06.y1 NCI.CGAP.Ma
gb_est43:BF167693	+	211.50	406.65	337	! BF167693 xn47g09.x1 Soares.NHCE
gb_est15:AI024617	+	210.00	402.23	389	! AI024617 ov52f10.x1 Soares_test
gb_est84:BF143048	+	168.00	312.96	765	! BF143048 601788733F1 NCI.CGAP.L
gb_est10:W21436	+	157.00	297.86	412	! W21436 zb52a06.r1 Soares.fetal
gb_est8:AA488780	+	152.50	290.45	360	! AA488780 aa54c10.r1 NCI.CGAP.GC
gb_est49:AW582560	+	146.00	284.26	192	! AW582560 RC1-SP0278-080100-011
gb_est72:BE289243	+	135.00	250.06	830	! BE289243 601092806F1 NCI.CGAP.M
gb_est84:BF137533	+	134.50	245.95	877	! BF137533 601780533F1 NCI.CGAP.L
gb_est42:AW52200	+	128.00	246.57	243	! AW52200 wy87c04.x1 Soares.NSF
gb_est81:BE937452	+	116.50	228.72	0.0013	! BE937452 RC1-SP0278-310800-019
gb_est89:BF551964	+	110.50	205.34	475	! BF551964 UI-R-C27-09-0-UI
gb_est95:BG008010	+	110.00	204.85	0.0272	! BG008010 QV4-GN0314-281100-607
gb_est100:BG387377	+	110.00	199.78	0.0522	! BG387377 602456143F1 NIH.MGC.15
gb_est80:BE844375	+	108.50	196.76	0.0768	! BE844375 EST119 Apis mellifera
gb_est4:AA240232	+	107.00	199.54	0.0538	! AA240232 my24b02.r1 Barstead mc
gb_est83:BF130765	+	106.00	190.68	0.1676	! BF130765 601818408F1 NIH.MGC.58
gb_est83:BF128614	+	105.50	194.61	0.1013	! BF128614 601810869F1 NIH.MGC.48
gb_est49:AW634441	+	105.50	194.49	0.1028	! AW634441 bl20g09.w1 Blackshear

gb_est97:BG167387 + 105.50 188.30 0.2273 954 ! BG167387 602342635F1 NIH.MGC

gb_est93:BF876874 + 105.00 195.92 0.0855 417 ! BF876874 PM4-ET0154-151100-0

gb_est48:AW555889 - 105.00 192.67 0.1297 570 ! AW555889 L0260G12-3 Mouse Ne

gb_est26:AI893253 - 104.50 187.03 0.2676 893 ! AI893253 me29e08.y1 Soares m

seq_name: gb_est102:BG609411

seq_documentation_block:

LOCUS BG609411 556 bp mRNA EST 17-APR-2001

DEFINITION 323251 MARC LPIG Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BG609411

VERSION BG609411.1 GI:13659390

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 556)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

JOURNAL Unpublished (2000)

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCCAGTCACGACG

Plate: 98 row: P column: 8

Seq primer: ATTAGGTGACACTATAG.

FEATURES

Location/Qualifiers

1..556

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="MARC LPIG"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from day 11, 13, 15, 20,

and 30 embryos."

BASE COUNT 139 a 153 c 141 g 123 t

ORIGIN

alignment_scores:

Quality: 708.00 Length: 130

Ratio: 5.488 Gaps: 0

Percent Similarity: 99.231 Percent Identity: 97.692

alignment_block:

US-09-457-066-2_COPY_210_345 x BG609411

Align seg 1/1 to: BG609411 from: 1 to: 556

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
|||||
167 CTGACTTAGAATCTATACAGGCCAATGGCACTGTCGCAAGGC 216

17 apbeValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
|||||

217 TTTTGTTCGGAGAGAAATCCAGAGTGGTGGATCTGAACCTTCTCAAG 266
|||||

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
|||||

267 AACAACTGAGGCTATACAGCTGCACCCCTAGGAACTTTTCACTCTATC 316
|||||

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51  ArgGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67
|||||
317 AGGGAAGAGCTGAAGAGAACAGACACATCTTCTGGCCAGGCTGCCCT 366
|||||
67  uValLysArgCysGlyGlyAsnCysAlaCysLeuHisAsnCysAsnG 84
|||||
367 CGTCAAGCGTTGTGGCGGGAACGTGCTGCTGCATGCACACCTGCAATG 416
|||||
84  luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
|||||
417 AGTGTCAAGTGTCTCCCGCAGCAAGTACCAAGAAATATCAGAGGTCCTT 466
|||||
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
467 CAGTTGAGACCCCAAGACAGGTGTCCGGGGGTGCACAAAGTCCCTCACCGA 516
|||||
117 pValAlaLeuGluHisGluGluCysAspCysValCys 130
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517 CGTGGCCCTGGACACACAGGAGGTGTGACTGCGTGTGC 556
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seq_name: gb_est81:BE958470

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seq_documentation_block:
LOCUS BE958470 523 bp mRNA EST 04-OCT-2000
DEFINITION 601644787F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930045 5',
mRNA sequence.
ACCESSION BE958470
VERSION BE958470.1 GI:10569175
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM763 row: m column: 22
High quality sequence start: 2
High quality sequence stop: 513.
Location/Qualifiers
1..523
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3930045"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: brain; Vector: pONR-LIB (Clontech); Site_1:
SfiI (ggccctcgcc); Site_2: SfiI (ggccatggcc);
Double-stranded cDNA was prepared from cell line RNA.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 147 a 118 c 129 g 128 t 1 others
ORIGIN

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alignment_scores:
Quality: 705.00 Length: 136
Ratio: 5.261 Gaps: 0
Percent Similarity: 98.529 Percent Identity: 97.794

alignment_block:
US-09-457-066-2_COPY_210_345 x BE958470 ..
Align seg 1/1 to: BE958470 from: 1 to: 523
1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
:::|||||
103 GTGGAGCTTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGGCAAGC 152
|||||
17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
|||||
153 TCTCTGTTTCGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 202
|||||
34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
|||||
203 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 252
|||||
51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67
|||||
253 AGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCT 302
|||||
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
|||||
303 GGTAAACGCTGTGTGGGAACCTGTGCGCTGNTGTCTCCACAAATTGCAATG 352
|||||
84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
|||||
353 AATGTCAATGTGTCCAAAGCAAGTTACTAAAAAATACCACGAGTCTCTT 402
|||||
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
403 CAGTTGAGACCCCAAGACCGGTGTGAGGGGATTCACAAATCACTCACCGCA 452
|||||
117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134
|||||
453 CGTGGCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 501
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134 hrGlyGly 136
502 CAGGAGGA 509

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seq_name: gb_est82:BF021679

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seq_documentation_block:
LOCUS BF021679 523 bp mRNA EST 29-DEC-2000
DEFINITION uy50f05.y1 NCI-CGAP_Lu30 Mus musculus cDNA clone IMAGE:3663009 5',
similar to TR:Q9QY71 Q9QY71 FALLOTEIN.; mRNA sequence.
ACCESSION BF021679
VERSION BF021679.1 GI:10753011
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

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alignment_scores:
  Quality: 663.00      Length: 133
  Ratio: 5.140         Gaps: 0
  Percent Similarity: 96.992  Percent Identity: 87.218

alignment_block:
  US-09-457-066-2_COPY_210_345 x BF151355  ..

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1  LeuAspLeuGluAAspLeuTyArgProThrTrpGlnLeuLeuGlyLysAl 17
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
163 GTGGACTTGGACGACGCTCTACAAGCCAACTGGCAGCTTTTGGGCAAGGC 212

17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
213 TTTCTCTGTATGGGAAAAAGCAAGAGTGGTGAATCTGAATCTCTCAAGG 262

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
263 AAGAGTAAACTCTACAGCTGCACACCCGGAACTTCTCAGTGCCATA 312

51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
313 CGGGAAGAGCTAAAGAGGACAGATACCATATTCCTGGCCAGGTGTCTCCT 362

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

51 ArfGGuGuLeuLysArgThrAspThrIlePheIlePrProGlyCysLeuLe 67
|||||
313 CGGGAAAGACTAAAGAGGACAGATACCATATTCCTGGCCAGGTGTCTCCT 362
67 uVallysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

363 GGTCAAGCGCTGTGGAGGAATTTGCTGTGTCTCCATAATTGCAATG 412

84 lUcYsGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

413 AATGTCAGTGTCTCCACATAAGTTACAAAAAGTACCATGAGTCCCTT 462

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117

463 CAGTTGAGACCAAACTCGAGTCAAGGATTGCATAAAGTACTCAATGA 512

117 pValalaLeuGluHisHisGluCysAspCysValCysArgGlySer 133

513 TGTGCTCTTGAACACACACAGGAATGTGACTGGGTGTGTAGAGGGAAC 561

seq_name: gb_est83:BF102859

seq_documentation_block: 851 bp mRNA EST 19-OCT-2000
LOCUS BF102859 601646827F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4073095 5',
DEFINITION mRNA sequence.

ACCESSION BF102859

VERSION BF102859.1 GI:10885385

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 851)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: CLONETECH Laboratories, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM921 row: f column: 08

High quality sequence stop: 529.

FEATURES

source

1. 851

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4073095"

/clone_lib="NIH_MGC_60"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);

Site_1: SfII (ggcgcctggcc); Site_2: SfII (ggcattatggcc

); Double-stranded cDNA was prepared from cell line RNA.

5' and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-ATCTAGAGCGGAGCGGCACATG-dt(30)BN-3'

(where B = A, C, G and N = A, C, G, or T). Average

insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA). Note: this is a NIH-MGC

Library."

BASE COUNT 234 a 169 c 238 g 210 t

ORIGIN

alignment_scores:

Quality: 622.00 Length: 138

Ratio: 4.712 Gaps: 4

Percent Similarity: 95.652 Percent Identity: 93.478

alignment_block:

US-09-457-066-2_copy_210_345 x BF102859

Align seg 1/1 to: BF102859. from: 1 to: 851

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17

149 TTGACATTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGCAAGGC 198

17 aPheVal.PheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr 33

199 T...TTGTTTTTGGAAAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACA 245

34 GluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIl 50

246 GAGGAGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCAT 295

50 eArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuL 67

296 AAGGAAGAACTAAGAGAACCGATACCACTTTCTGGCCAGGTTGTCTCC 345

67 euValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 83

346 TGGTTAAACGCTGTGGTGGGAACGTGCTG. TGTCTCCACAATTGCAAT 394

84 GluCysGlnCysValProSerLysValThrLysLysTyrHisGluValLe 100

395 GAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGGTCCT 444

100 uGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrA 117

445 TCAGTTAGACCAAGAACCGGTGTCAGGGGATG.CACAAATCACTCACCG 493

117 spValalaLeu.GluHisHisGluGluCysAspCysValCysArgGlyse 133

494 ACCTG...GCCTGAGCACCATGAGGAGTGTGACTGTGTGTCGAGGGAGC 540

133 rThrGlyGly 136

541 CACAGGGGGA 550

seq_name: gb_est98:BG243001

seq_documentation_block:

LOCUS BG243001 910 bp mRNA EST 13-FEB-2001

DEFINITION 602355974F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483938 5',

mRNA sequence.

ACCESSION BG243001

VERSION BG243001.1 GI:12752725

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 910)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10323 row: d column: 19

High quality sequence stop: 690.

FEATURES

Location/Qualifiers

1. 910

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4483938"

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/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NCI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
242 a 220 c 250 g 198 t
BASE COUNT
ORIGIN

```

alignment_scores:			
Quality:	606.00	Length:	136
Ratio:	4.591	Gaps:	0
Percent Similarity:	97.059	Percent Identity:	87.500

alignment_block:

US-09-457-066-2 COPY 210 345 x BG243001 alignment_block:

Align seg 1/1 to: BG243001 from: 1 to: 910

1 LeuAspLeuCluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
::: : ::::: :
108 GTGGACTGGACAGCCCTTCACAACCACATGGGCAGCT TTTGGGCAAGGC 156

17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
::: : ::::: :
157 TTTTCCTGTATGGGAAAAAAGCAAAGTGTCGAATCTGAATCTCCTCAAGG 206

34	lucluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle	50
	
207	AAGAGGTAAAACCTCTCAGCTGCACACCCCGAACTTCTCAGTGTCCATA	256
51	ArgGluCluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLeu	67
257	CGGGAAAGAGCTAAAGAGGACAGATACCATAATCTGGCCAGGTTGTCTCCT	306

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
 |||||
 307 GGTCAGCGCGTGTGGAGGAAA.TGTGCTGTTGTCTCCATAATTGCAATG 355

84 luCysGlnCysValproSerLysValThrLysLysTyrHisGluValLeu 100
|||||
356 AATGTCAGTGTGTCCACGATAAGTTACAAAAAGTACCATGAGGTCTT 405

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
 |||||
 406 CAGTTGAGACCAAAACATGA.GTCAAGGGATTGCATAGTCACTCACTGA 454

117 pvalalaLeucluhHisHISgluCysAspCysValCysArgGlySert 134
|||||
455 TGTGCTCTGGAAACCCAGGGAATGTACTGTGTGTAGAGGAAACG 504

134 hrGlvGly 136

505 CAGGAGGG 512

seq_name: qb_est82:BF011835

seq documentation block:

LOCUS	BF011835	447 bp	mRNA	EST	06-OCT-2000
DEFINITION	us37d10.y1 Soares_NNEBA_branchial_arch Mus musculus cDNA clone IMAGE:3169267 5' similar to TR:Q9QY71 Q9QY71 FALLOTEIN. ; mRNA sequence				

Accession
BF011835
Version
BF011835.1
Keywords
EST
Sequence:
GI:10712110

REFERENCE
SOURCE
ORGANISM

REFERENCE:
1 (bases 1 to 447)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS	JOURNAL
TITLE	COMMENT
...	...

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonana
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1064727

Seq primer: -40RP from Gibco
High quality sequence stop:

FEATURES
SOURCES

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Location/Qualifiers
1. .447
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3169267"
/clone_lib="Soares_NNEBA"
/tissue_type="branchial"
/dev_stage="embryo 10 5

```

```
/set-beag="DH10B" (phage resistant) "
/note="vector: pT7D3-pac (Pharmacia) with a modified
polylinker; Site1: NotI; Site2: EcoRI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGTCGGAGCCGCATCATTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7D3 vector. Library
constructed and normalized by Bento Soares and M.Patima
Bonaldo."
```

BASE COUNT	126 a	104 c	108 g	109 t
ORIGIN				

alignment_scores:

Quality:	587.00	Length:	116
Ratio:	5.149	Gaps:	0
Percent Similarity:	98.276	Percent Identity:	88.793

alignment block:

US-09-457-066-2_COPY 210 345 x BF011835

Align seq 1/1 to: BF011835 from: 1 to: 447

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAla 17
 100 GTGGACTTTGGACAGCCTCTACAAGCCAAACATGCGAGCTTTTGGCAAGC 149
 17 apheValPheGlyArgLysSerArgValValAsnLeuLeuThrG 34
 150 TTTCTGTATGGAAAAAAGCAAGTGGTGAATCTCCTCAAGS 199
 34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
 200 AAGAGTAAACTCTACAGTTCACACCCGGACATCTCAGTCCCA 249

51 ArgGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
 |||||
 250 CGGGAAGAGCTAAAGAGGACAGATACCATATCTGGCCAGGTTGTCCT 299

67 uVallysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
300 GGTCAGCGCTGTGCAGGAATTTCTGCTCTTCTCTCCATAATTTCACATC 349

84 LuCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
350 AATGFCAGTGTCGCCACCTACAAAGTACCATTGACGGCTTT 399

[illegible]

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 116
 400 CAGTTGAGACCAAAAGCTGGAGTCAAGGGATTGCATAAATCACTCACT 447

seq_name: gb_est28:AL047637

seq_documentation_block: 304 bp mRNA EST 01-MAR-2000
 LOCUS AL047637
 DEFINITION DKFZp586J0421_r1 586 (synonym: hutel) Homo sapiens cDNA clone
 DKFZp586J0421, mRNA sequence.
 ACCESSION AL047637
 VERSION AL047637.1 GI:4728633
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 304)
 AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
 Wiemann,S.
 TITLE EST (Ottenwaelder, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Ottenwaelder B
 MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix* (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No sl sequence
 available.

This clone (DKFZp586J0421) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source

1..304
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZp586J0421"
 /clone.lib="586 (synonym: hutel)"
 /tissue_type="uterus"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI/MluI"

BASE COUNT 86 a 68 c 80 g 70 t

alignment_scores:
 Quality: 568.00 Length: 101
 Ratio: 5.524 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.010

alignment_block:
 US-09-457-066-2_COPY_210_345 x AL047637

Align seg 1/1 to: AL047637 from: 1 to: 304

34 GluGluValArgLeuTyrSerCysThrProArgAsnPheserValSer11 50

2 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCAT 51

50 eArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuL 67

52 AAGGAGAGAACTAAAGAACCCGATACCAATTTCTGGCCAGGTTGTCTCC 101

67 euValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 83

102 TGGTTAAACGCTGTGTGGGAAGTGTGCTGTGTCTCCACAAATTCGAAT 151

84 GluCysGlnCysValProSerLysValThrLysLysTyrHisGluValLe 100

152 GAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCT 201

100 uGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 117
 117 spValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySer 133
 252 ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGC 301
 134 Thr 134
 ...
 302 TCA 304

seq_name: gb_est91:BF670092

seq_documentation_block: 874 bp mRNA EST 21-DEC-2000
 LOCUS BF670092
 DEFINITION 602119417F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276493 5',
 mRNA sequence.
 ACCESSION BF670092
 VERSION BF670092.1 GI:11943987
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 874)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cygabs-remail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC1097 row: a column: 06

High quality sequence stop: 598.

FEATURES

source

1..874

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="NIH_MGC_56"

/tissue_type="primitive neuroectoderm"

/lab_host="DH10B (T1 phage-resistant)"

/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:

SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc);

Double-stranded cDNA was prepared from cell line RNA. 5'

and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGCGGCGGCGCATG-GT(30)BN-3',

(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA)."

BASE COUNT 227 a 208 c 245 g 194 t

ORIGIN

alignment_scores:

Quality: 538.50 Length: 143

Ratio: 4.240 Gaps: 10

Percent Similarity: 88.811 Percent Identity: 86.713

alignment_block:

US-09-457-066-2_COPY_210_345 x BF670092

Align seg 1/1 to: BF670092 from: 1 to: 874

```

1  LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
|||||
19 TTGGACTTAGAAGACTATATAGCCAACTTGGCAACTTCTTGGCAAGGC 68
|||||
17 aPheValPhe.GlyArgLysSerArgValValAspLeuAsnLeuLeuThr 33
|||||
69 TTGG...TTTGGGAAGAAATCCAGAGTGGTGATCTGGAACCTTCTAACA 115
|||||
34 GluGluValArgLeu..TyrSerCysThrProArgAsnPheSerValSer 49
|||||
116 GAGGAGTAAGATTATAGCATGTGTGCACACCTCGTAACCTTCTCAGTGTCC 165
|||||
50 IleArg.GluGluLeuLysArgThrAspThrIle.PheTrpProGlyCys 65
|||||
166 ATAATGGGAAGAACTAAAGAGAACCGATACCATGTTCTTGCCAGGTTGT 215
|||||
66 LeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCy 82
|||||
216 CTCCTGGTTAAACGCTGTGTGGGAACGTGCTGTGTGTCTCCAAATG 265
|||||
82 sAsnGluCysGln.CysValProSerLysValThrLysLysTyrHis.Gl 98
|||||
266 CAATGAATGTCAGTGTGTCCCAAGCAAGTTACTAAAAATACCAGCGA 315
|||||
98 uValLeuGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerL 115
|||||
316 GTGCTCTCAGTGTGAGACCAAGACCGGTGTGAGGATGGCACAATCAC 365
|||||
115 euThrAspValAlaLeuGluHis.HisGlu.GluCysAspCys.ValCys 130
|||||
366 TCACCCAGCTGGCCCTGGAGCACCATGAGAGTGTGTGTGTGTGTGTG 415
|||||
131 ArgGlySerThr 134
|||||
416 AGAGGGAGGCACA 427

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seq_name: gb_est82:BF031624

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seq_documentation_block: 950 bp mRNA EST 10-OCT-2000
LOCUS BF031624
DEFINITION 601558104F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827760 5',
mRNA sequence.
ACCESSION BF031624
VERSION BF031624.1 GI:10739336
KEYWORDS EST.
SOURCE human.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM497 row: h column: 01
High quality sequence stop: 415.
Location/Qualifiers
1..950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3827760"
/clone_lib="NIH_MGC_58"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"

```

```

FEATURES
source
Location/Qualifiers
1..950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3827760"
/clone_lib="NIH_MGC_58"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"

```

```

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 288 a 309 c 211 g 142 t
ORIGIN

```

```

alignment_scores:
Quality: 523.00 Length: 95
Ratio: 5.564 Gaps: 0
Percent Similarity: 98.947 Percent Identity: 97.895

```

```

alignment_block:
US-09-457-066-2_COPY_210_345 x BF031624

```

Align seg 1/1 to: BF031624 from: 1 to: 950

```

42 ThrProArgAsnPheSerValSerIleArgGluLeuLysArgThrAs 58
|||||
3 ACACCTCGTAACCTCTCAGTGTCCATAAGGAAGAACTAAAGAGAACCGA 52
|||||
58 pThrIlePheTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsn 75
|||||
53 TACCATTTTCTGGCCAGGTGTCTCTCTGTTAAACGCTGTGTGGGAAC 102
|||||
75 ysAlaCysCysLeuHisAsnCysAsnGluCysGlnCysValProSerLys 91
|||||
103 GTGCTGTCTCTCCACAAATGCAATGAATGTCATGTGCCCAAGCAA 152
|||||
92 ValThrLysLysTyrHisGluValLeuGlnLeuArgProLysThrGly 108
|||||
153 GTTACTAAAAATACCACGAGGTCTTCAGTTGAGACCAAGACCGGTGT 202
|||||
108 lArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisGluG 125
|||||
203 CAGGGGATTGCCAAATACATCACCGACGTGGCCCTGGAGCACTATGAG 252
|||||
125 luCysAspCysValCysArgGlySerThrGlyGly 136
|||||
253 AGTGTGACTGTGTGTGCAGAGGAGGACAGGAGGA 287

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seq_name: gb_est97:BG118707

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seq_documentation_block: 968 bp mRNA EST 30-JAN-2001
LOCUS BG118707
DEFINITION 602348280F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4443498 5',
mRNA sequence.
ACCESSION BG118707
VERSION BG118707.1 GI:12612213
KEYWORDS EST.
SOURCE human.

```

ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM10217 row: 0 column: 19

High quality sequence start: 8

High quality sequence stop: 574.

FEATURES

Location/Qualifiers

1..968

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:443498"

/clone_lib="NIH_MGC_90"

/tissue_type="adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 313 a 230 c 219 g 206 t

ORIGIN

alignment_scores:

Quality: 507.00 Length: 136

Ratio: 4.694 Gaps: 1

Percent Similarity: 79.412 Percent Identity: 79.412

alignment_block:

US-09-457-066-2_copy_210_345 x BG118707 ..

Align seg 1/1 to: BG118707 from: 1 to: 968

1 LeuAspLeuGluAspLeuTyrArgProThrGlnLeuLeuGlyLysAl 17

174 TTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGC 222

17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

223 .TTTGTGTTTGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAG 272

34 LuGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

273 AGGA..... 276

51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67

277GGTGTCTCCT 287

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

288 GGTAAACGCTGTGGGAACCTGTGCTGTCTCCACAATTCGAATG 337

84 LuCysGlnCysValProSerLysValThrLysLysThrHisGluValLeu 100

338 AATGTCATGTCTCCCAAGCAAGTTACTAAATAATACCAGAGGTCCTT 387

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117

388 CAGTTGAGACCAAGACCGGTGTCTCAGGGGATTCACAAATCACTCACCGA 437

117 pValalaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134

438 CGTGGC.CTGGAGCACCATTGAGGAGTGTGACTGTGTGTCAGAGGGAGCA 486

134 hrGlyGly 136

487 CAGGAGGA 494

seq_name: gb_gss3:CNS024MX

seq_documentation_block:

LOCUS CNS024MX 877 bp DNA GSS 12-MAY-2000

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone

235A22 of library G from Tetraodon nigroviridis, genomic survey sequence.

AL180978

VERSION AL180978.1 GI:7819035

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 877)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 877)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 877)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

FEATURES

Source

1..877

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="235A22"

/clone_lib="G"

/note="Genoscope sequence ID : COAG235BAL1SP1-end : PUC-Ori"

BASE COUNT 229 a 207 c 188 g 248 t 5 others

alignment_scores:

Quality: 439.50 Length: 270

Ratio: 3.632 Gaps: 4

Percent Similarity: 44.815 Percent Identity: 34.444

alignment_block:

US-09-457-066-2_COPY_210_345 x CNS024MX/rev ..

Align seg 1/1 to reverse of: CNS024MX from: 1 to: 877

1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17

845 GTGGATATGGAGGAGTGTACAACCATCTCGCATGTGCKGGGGAAGTC 796

17 aPheValPheGlyArgLysSerArg.Val..... 26

795 ATTCATCCATAGTAAAAAAGCCAGAGGTAGGACATTTTCAGATGGACTCCC 746

26 26

745 GACAAGGAACCTATATGTTGGGGCAGAGTTTACAGAAAGKTCACACAC 696

27ValAspLeu.AsnLeuLeuThr 33

695 CTTTCTTCTTATGCTCTTTTTCAGGAGGAGGAGATCTTTTAACTCTGCTGAGG 646

34 GluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

.....

645 GATGAAGTGGCAGCTGTACAGCTGCACACCGGCGCAACTTCTCTGTGTCTTT 596

50 eArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuL 67
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
595 GCCTGAGGAGCTGAAGAGGACCGATGTAATTTCCTGGCCAAGCTGCCCTCC 546

67 euValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
545 TGGTGAATCCCTGTGGCGGAACCTCGCGCTGCTGCTCATCCGCTGCCTAC 496

84 GluCysGlnCysValProSerLysValThrLysLysTyrrHisGlu..... 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
495 GACTGCCAGTGCGTTCCCACCAGGGTCACGAAGAATAATCATGAGGTAAA 446

98 98

445 TGCTAGCACCTTCACTTGAGGATGATGTTTCGTTTTGCTGCCCTTTTAA 396

98 98

395 AAGATTTTGAAATCGCGGTTTGAACCTTCACAATTTTGTCTGTGCCAATT 346

98 98

345 ACACAATACTACAATKCCAGACACTGTGAAATGTACAAATACTTTATCTGA 296

98 98

295 GCTTGAAAAATTGAGATCTGAGAGCAAATCCACTTACACTGCAATATTTG 246

98 98

245 TTTTAATACAAACAAATCAACAATCAAGACCAAGCTAAATGCAATTT 196

98 98

195 GATCGATAATATGATCAGTTTAAAGATGAAATGTTTGTATGTCCAAACAATG 146

99 ValLeuGlnLeuArgProLysThrGlyValargGlyLeuHisL 113
||||| ||||| :|||: |||: |||: |||: |||: |||: |||: |||: |||:
145 TTGTGAGTTTCTGCTGTAACATTCGAAATGGTGGCAAGGCCCTGCAGA 96

113 ysserLeuThrAspValAlaLeuGluHisHisGluGluCysAspCysVal 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
95 AATCGTTGACCGAGCTGCCCTTAGAACACACAGAAATGCCCTTGGCGTG 46

130 CysArg 131
|||::

45 TGTAAA 40

seq_name: qb_est84:BF163629

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seq_documentation_block:
LOCUS       BF163629                902 bp    mRNA          EST
DEFINITION  601769732F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3989215 5',
            mRNA sequence.
ACCESSION   BF163629
VERSION     BF163629.1  GI:11044002
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 902)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-femail.nih.gov
            Tissue procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.

```

```

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9198 row: o column: 08
High quality sequence stop: 743.
FEATURES
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        Location/Qualifiers
            1..902
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                /strain="CZECH II (feral)"
                /db_xref="taxon:10090"
                /clone="IMAGE:3989215"
                /clone_11b="MCI-CGAP-Lu29"
                /tissue_type="spontaneous tumor, metastatic to mammary.
                Stem cell origin."
                /lab_host="DH10B"
                /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sali;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dm.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"
            248 a 203 c 241 g 210 t
            BASE COUNT
            ORIGIN

alignment_scores:
    Quality: 381.00 Length: 69
    Ratio: 5.603 Gaps: 0
    Percent Similarity: 98.551 Percent Identity: 92.754

alignment_block:
    US-09-457-066-2_COPY_210_345 x BF163629 ..
    Align seg 1/1 to: BF163629 from: 1 to: 902

68 ValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnCl 84
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7 GTCCGGCGCTGGGAGGAATTTGCCTGTTCTCCATAATTCGAATGA 56

84 uCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeuG 101
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57 ATGTCAAGTGTGTCACCAGTAAAGTTACAAAAAGTACCATGAGGTCCTTC 106

101 InLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAsp 117
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
107 AGTTGAGACCAAAAACTGGAGTCAAGGGATTGCATAAGTCACTCACTGAT 156

118 ValAlaLeuGluHisHisGluCluCysAspCysValCysArgGlySerTh 134
...:||||:||||:||||:||||:||||:||||:||||:||||:||||:
157 GTGGCTCTGGACACACCAGGAGGAATGTGACTGTGTGTAGAGGAACGC 206

134 rGlyGly 136
:|||||
207 AGGAGG 213

seq_name: gb_htc:AK003359

seq_documentation_block:
LOCUS AK003359 1796 bp mRNA HTC 08-FEB-2001
DEFINITION Mus musculus 18 days embryo cDNA, RIKEN full-length enriched
library, clone:1110003109, full insert sequence.
ACCESSION AK003359
VERSION AK003359.1 GI:12833975
KEYWORDS CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,
clone_11b:RIKEN full-length enriched mouse cDNA library
clone:1110003109.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Methods Enzymol. 303, 19-44 (1999)
REFERENCE
2 (sites)

```


COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:898546
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 283.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1365326"
 /clone_lib="Soares_mammary_gland_NbMMG"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)
 primer 15'
 TGTTCACCAATCTGAATGGGAGCGCGCAATGGTTTTTTTTTTTTTTTTTT
 T 3'; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT7T3 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. library
 constructed and normalized by Bento Soares and M.Fatima
 Bonaldo."

BASE COUNT 82 a 81 c 81 g 80 t
 ORIGIN

alignment_scores:

Quality: 327.00 Length: 71
 Ratio: 4.739 Gaps: 0
 Percent Similarity: 97.183 Percent Identity: 83.099

alignment_block:

US-09-457-066-2_COPY_210_345 x AI020581 ..

Align seg 1/1 to: AI020581 from: 1 to: 324

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 :::::::::::::::::::::::::::::::::::::::::::::::::::::
 112 GTGGACTTGGACAGCCTCTACAGCAACATGGCAGCTTTTGGCAAGGC 161
 17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuThrG 34
 :::::::::::::::::::::::::::::::::::::::::::::::::::::::
 162 TTTTCTGTATGTGAAAAAAGCAAGTGGTGAATCTGAATCTCCTCAAGG 211
 34 iuGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
 :::::::::::::::::::::::::::::::::::::::::::::::::::::::
 212 AAGAGGTAAACTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCATA 261
 51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuIe 67
 :::::::::::::::::::::::::::::::::::::::::::::::::::::::
 262 CGGAAGAGCTAAGAGAGACAGATACCATATTCTGGCCAGGTGTCTCCT 311
 67 uValLysArgCys 71
 :::::::::::::::::::::
 312 GGTCAAGCGCTGT 324

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2001, 01:12:39 ; Search time 50.8 Seconds

(without alignments)

162.300 Million cell updates/sec

Title: US-09-457-066-2_COPY_210_345

Perfect score: 754

Sequence: 1 LDLELDYPTWQLLKAFV.....DVALEHHECDVCRGSTGG 136

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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Pred. No. is the number of results, predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	100.0	318	21	AA1984558
2	754	100.0	339	21	AA198438
3	754	100.0	345	20	AA1933679
4	754	100.0	345	20	AA191766
5	754	100.0	345	20	AA1930023
6	754	100.0	345	21	AA1948557
7	754	100.0	345	21	AA194250
8	754	100.0	345	21	AA194322
9	754	100.0	345	21	AA190633
10	754	100.0	345	21	AA190634
11	754	100.0	345	21	AA190635
					A fragment of plat
					Lung cancer associ
					Human VEGF-E prote
					Human PRO200 prote
					Human vascular end
					Human zvegf3, SEQ
					Human platelet-der
					Human PRO200 (UNQ1
					Human RACE generat
					Human VEGF-X homol
					Human VEGF-X prote

12	754	100.0	345	21	AA190636	Human VEGF-X prote
13	754	100.0	345	21	AA190644	Human VEGF-X prote
14	754	100.0	345	21	AA190650	Human 990126veg p
15	754	100.0	345	21	AA190651	Human VEGF-X prote
16	754	100.0	345	21	AA191978	Human PRO200 (vasc
17	754	100.0	345	21	AA1933414	Human PRO200 prote
18	754	100.0	345	21	AA1924412	Human PRO713 prote
19	754	100.0	345	21	AA1901419	Human TANGO 128.
20	754	100.0	345	21	AA1903003	Human growth facto
21	754	100.0	345	21	AA190658	Human growth facto
22	754	100.0	345	21	AA194557	Amino acid sequenc
23	754	100.0	345	21	AA195285	Bone morphogenic p
24	754	100.0	345	22	AA195080	Human PRO200 prote
25	754	100.0	345	22	AA194995	Human PRO200 prote
26	754	100.0	345	22	AA1953074	Human anglogenesis
27	754	100.0	374	21	AA190639	Human VEGF-X prote
28	744	98.7	354	21	AA190640	Human VEGF-X prote
29	744	98.7	354	21	AA190641	Human VEGF-X prote
30	697	92.4	345	21	AA194858	Mouse zvegf3, SEQ
31	697	92.4	345	21	AA194861	Murine vascular en
32	697	92.4	345	21	AA194559	A murine platelet-
33	646	85.7	149	21	AA190642	Human VEGF-X PDGF-
34	607	80.5	113	21	AA190631	Human VEGF-X prote
35	607	80.5	113	21	AA190632	Human VEGF-X prote
36	590.5	78.3	227	21	AA190637	Human VEGF-X prote
37	590.5	78.3	227	21	AA190638	Human VEGF-X prote
38	346.5	46.0	282	21	AA190653	Human VEGF-X prote
39	345.5	45.8	370	21	AA194863	Mouse growth facto
40	344.5	45.7	322	21	AA191129	Human Platelet Der
41	344.5	45.7	370	21	AA194853	Human growth facto
42	344.5	45.7	370	21	AA194864	SEQ. ID. 37 from W
43	344.5	45.7	370	21	AA191130	Human Platelet Der
44	344.5	45.7	370	22	AA190888	Human VEGF-G prote
45	343.5	45.6	370	22	AA190895	Human VEGF-G prote

ALIGNMENTS

RESULT 1

AA194558
ID AA194558 standard; Protein; 318 AA.

XX AA194558;

XX 25-JUL-2000 (first entry)

XX A fragment of platelet-derived growth factor C (PDGF-C).

XX Platelet-derived growth factor C; PDGF-C; cell proliferation;
XX growth factor; heparin; connective tissue; wound healing; VEGF-F;
XX fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
XX choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
XX lung carcinoma; erythroleukemia; tissue remodelling.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 287 /note= "encoded by AAS"

XX WO200018212-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US22668.

XX 30-SEP-1998; 98US-0102461.

XX 12-NOV-1998; 98US-0108109.

XX 03-DEC-1998; 98US-0110749.

XX 18-DEC-1998; 98US-0113002.

XX 21-MAY-1999; 99US-0135426.

XX 15-JUL-1999; 99US-0144022.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
XX Eriksson U, Aase K, Lee X, Ponten A, Dutela M, Alitalo K;
PI Oestman A, Heldin C, Betsholtz C;
XX
XX WPI; 2000-292954/25.
DR N-PSDB; AAA12524.
XX
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PT receptor
XX
XX Disclosure; Fig 4; 135pp; English.
XX
XX The present sequence represents a human platelet-derived growth factor C
CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have
CC the ability to stimulate and enhance proliferation or differentiation,
CC and/or growth or motility of cells expressing a PDGF-C receptor.
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC be used for stimulating connective tissue or wound healing. The
CC PDGF-C polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC remodelling during invasion of tumour cells into a normal population of
CC cells. Antagonists can also be used to treat fibrotic conditions,
CC especially found in the lung, kidney or liver.
XX
XX Sequence 318 AA;
SQ

Query Match 100.0%; Score 754; DB 21; Length 318;
Best Local Similarity 100.0%; Pred. No. 4.3e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEEVRLYSCTPRNFSVSIREELKRTDTI 60
Db 183 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEEVRLYSCTPRNFSVSIREELKRTDTI 242
Qy 61 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTVGRLGHLKSLTDVAL 120
Db 243 fwpgcilvkrcgncacclhncnecqvpksvktkyhevlqlrpkrtgvrghksltdval 302
Qy 121 EHHEECDCVCRGSTGG 136
Db 303 ehheecdcvcrgstgg 318

RESULT 2
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ID AAB58438 standard; Protein; 339 AA.
XX
XX AAB58438;
XX
XX 14-MAR-2001 (first entry)
XX
XX Lung cancer associated polypeptide sequence SEQ ID 776.
XX
XX Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX

OS Homo sapiens.
XX
XX W020005180-A2.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05918.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Ruben SM;
PI
XX
XX WPI; 2000-587514/55.
DR N-PSDB; AAF18314.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer
XX
XX Claim 11; Page 1305-1306; 1425pp; English.
XX
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX
XX Sequence 339 AA;
SQ

Query Match 100.0%; Score 754; DB 21; Length 339;
Best Local Similarity 100.0%; Pred. No. 4.6e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEEVRLYSCTPRNFSVSIREELKRTDTI 60
Db 204 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEEVRLYSCTPRNFSVSIREELKRTDTI 263
Qy 61 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTVGRLGHLKSLTDVAL 120
Db 264 fwpgcilvkrcgncacclhncnecqvpksvktkyhevlqlrpkrtgvrghksltdval 323
Qy 121 EHHEECDCVCRGSTGG 136
Db 324 ehheecdcvcrgstgg 339

RESULT 3
AA33679
ID AAY33679 standard; Protein; 345 AA.
XX
XX AAY33679;
XX
XX 11-JAN-2000 (first entry)
XX
XX Human VEGF-E protein.
XX

KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
 KW angiogenic disorder; age-related macular degeneration; vascular disease;
 KW neovascularization; tumor; gene mapping.

XX Homo sapiens.

XX WO9947677-A2.

XX 23-SEP-1999.

XX 10-MAR-1999; 99WO-US05190.

XX 17-MAR-1998; 98US-0040220.

XX 02-NOV-1998; 98US-0184216.

XX (GETH) GENENTECH INC.

XX Ferrara N, Kuo SS;

XX WPI; 1999-580306/49.

XX N-PSDB; AAZ23691.

XX New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy

XX Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to
 CC screen for antagonists and agonists, and the antagonists administered to
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
 CC age-related macular degeneration. It can be used to generate antibodies,
 CC useful therapeutically as antagonists, as above. The antibodies are also
 CC useful to detect VEGF-E polypeptide, especially to diagnose
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
 CC vascular disease, or neovascularization associated with tumor formation),
 CC by contacting the antibody with a tissue sample and detecting formation
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
 CC tissue samples. They can also be used to diagnose a disease or
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
 CC sample. They may also be used to produce probes useful to detect related
 CC sequences or for gene mapping. This sequence represents the human VEGF-E
 CC protein described in the method of the invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 754; DB 20; Length 345;
 Best Local Similarity 100.0%; Pred. No. 4,7e-71;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYPTWQLGKAFVFGKSRVDNLNLTTEVRLYSCTPRNFSVIRELKRDTII 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 210 ldledlyrptwqlgkatfgrksrvdnlnteelvryscprfnfsvsireelkrtdti 269
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 FWPgcLLVkrCGGNCACCLHNCNCQCVPSKVTKKYHVEVLQRPKTVGRGLHKSLEFDVAL 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 270 fwpgcLLVkrCGGNCACCLHNCNCQCVPSKVTKKYHVEVLQRPKTVGRGLHKSLEFDVAL 329
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 EHHEECDCVCRGSTGG 136

DB 330 ehheecdcvcrgstgg 345
 |||||||||||||||||||
 RESULT 4
 AAY41766
 ID AAY41766 standard; Protein; 345 AA.
 XX
 AC AAY41766;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO200 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 PR 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 28-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.

PR 29-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.

PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI: 1999-551358/46.

DR N-PSDB; AAZ34296.

XX New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders

XX Claim 12; Fig 207; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AAZ33891, to
 CC AAZ34338, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 754; DB 20; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.7e-71;

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEVRLYSCTPRNFSVSIREELKRTDTI 60
 .
 Db 210 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEVRLYSCTPRNFSVSIREELKRTDTI 269
 Qy 61 FMPGCLLVKRCGNCACCLHNCNCCQVPSKVTKKYHEVLQLRPKTGYRGLHKSLTDVAL 120
 Db 270 fwpgccllvkrcgncacclhncnccqvpkvtkkyhevlqlrpkgtgvrghksltdval 329
 Qy 121 EHHEECDCVCRGSTGG 136
 Db 330 ehheecdvcrgstgg 345

RESULT 5

AAV30023

ID AAV30023 standard; Protein; 345 AA.

XX AAV30023;

AC AAV30023;

XX 11-OCT-1999 (first entry)

XX Human vascular endothelial growth factor related protein.

XX Vascular endothelial growth factor related protein; VEGF-R protein;

XX tissue growth inhibition; tumour growth; cancer; tissue growth;

XX angiogenesis; coronary artery blockage.

XX Homo sapiens.

XX WO9937671-A1.

XX 29-JUL-1999.

XX 26-JAN-1999; 99WG-US01574.

XX 31-AUG-1998; 98US-0098548.

XX 27-JUN-1998; 98US-0072635.

XX 05-JUN-1998; 98US-0088089.

XX 24-JUN-1998; 98US-0090544.

XX (ELIL) LILLY & CO ELI.

XX Dou S, Na S, Song HY;

XX WPI: 1999-458680/38.

XX N-PSDB; AAX86352.

XX A vascular endothelial growth factor related protein and related

XX polynucleotide, useful for identifying antagonists and binding

XX compounds

XX Claim 1; Page 56-58; 62pp; English.

XX The present sequence represents a vascular endothelial growth factor

XX related (VEGF-R) protein. VEGF-R can be used in assays to identify

XX compounds that bind to it or that antagonize its activity. VEGF-R

XX antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting

XX tissue growth. This is useful for inhibiting tumour growth and for

XX treating cancer. VEGF-R itself can be used to stimulate tissue

XX growth, angiogenesis and to treat coronary artery blockage. The

XX VEGF-R coding sequence can be used for the recombinant production of

XX the VEGF-R protein.

XX Sequence 345 AA;

XX Query Match 100.0%; Score 754; DB 20; Length 345;

XX Best Local Similarity 100.0%; Pred. No. 4.7e-71;

XX Matches, 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEVRLYSCTPRNFSVSIREELKRTDTI 60
 .
 Db 210 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTEVRLYSCTPRNFSVSIREELKRTDTI 269
 Qy 61 FMPGCLLVKRCGNCACCLHNCNCCQVPSKVTKKYHEVLQLRPKTGYRGLHKSLTDVAL 120
 Db 270 fwpgccllvkrcgncacclhncnccqvpkvtkkyhevlqlrpkgtgvrghksltdval 329
 Qy 121 EHHEECDCVCRGSTGG 136
 Db 330 ehheecdvcrgstgg 345

Db 210 ldledlyrptwllgkafvgrksrvvdlntlteevrlyscptprnfsvsireelkrttdt 269
 QY 61 FWPGCLLVKRCGNCACCLHNCQCVPKSKVTKYHEVLQRLPKTGVRGLHKSITDVAL 120
 Db 270 fwpqcllvkrccgncacclhncqcvpkskvtkyhevllqrlpdkgtvrglhksitdval 329
 QY 121 EHHEEDCVCRCSTGG 136
 Db 330 ehheecdvcrcgstg 345

RESULT 6
 AAB48657
 ID AAB48657 standard; Protein; 345 AA.
 AC AAB48657;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human zvegf3, SEQ ID NO:33.
 XX
 KW Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
 KW neovascularisation; tissue repair; proliferation; differentiation;
 KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
 KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
 KW immunomodulation; hepatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200066736-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 03-MAY-2000; 2000WO-US40047.
 XX
 PR 03-MAY-1999; 99US-0304216.
 PR 10-NOV-1999; 99US-0164463.
 PR 04-FEB-2000; 2000US-0180169.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 WPI; 2000-687541/67.
 N-PSDB; AAC81582.
 XX
 PT Growth factor homologs and the nucleic acids that encode them, useful
 e.g. for treating liver damage, ischemia, multiple sclerosis and
 PT Alzheimer's disease -
 XX
 PS Claim 48; Page 125-126; 143pp; English.
 XX
 CC The invention relates to the human growth factor homologue zvegf4
 CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
 CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)
 CC characterised by a PDGF cystine knot structure, and a CUB domain
 CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like
 CC activity, having mitogenic activity on fibroblasts, vascular smooth
 CC muscle cells and pericytes, and has also been shown to stimulate bone
 CC growth. The invention also relates to fusion proteins comprising human
 CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
 CC fusions; expression constructs and host cells comprising human zvegf4
 CC nucleic acids; the recombinant expression of human zvegf4; an antibody
 CC which binds to human zvegf4 or a fragment thereof; a method of activating
 CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a
 CC method of modulating the proliferation, differentiation, migration or
 CC metabolism of bone cells, comprising exposing bone cells to
 CC zvegf4-derived polypeptides; and a method of detecting a genetic
 CC abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived
 CC fragments may be used to stimulate tissue development or repair, or
 CC cellular differentiation or proliferation. They are particularly used for

CC the treatment or repair of liver damage, and may also be used to
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
 CC multiple sclerosis). Due to their osteogenic activity, they may be used
 CC in the treatment of periodontal disease and fractures. They may also be
 CC used to enhance expansion and mobilisation of haematopoietic stem cells
 CC and endothelial precursor stem cells, which may be useful in the
 CC treatment of ischaemia, in wound healing, and in the modulation of the
 CC immune system. The present sequence represents human zvegf3.
 XX
 SQ Sequence 345 AA;
 Query Match 100.0%; Score 754; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDLEDLYRPTWOLLGKAFVGRKSRVVLDNLNLTTEEVRLYSLCTPRNFSVSIREELKRTDTI 60
 Db 210 ldledlyrptwllgkafvgrksrvvdlntlteevrlyscptprnfsvsireelkrttdt 269
 QY 61 FWPGCLLVKRCGNCACCLHNCQCVPKSKVTKYHEVLQRLPKTGVRGLHKSITDVAL 120
 Db 270 fwpqcllvkrccgncacclhncqcvpkskvtkyhevllqrlpdkgtvrglhksitdval 329
 QY 121 EHHEEDCVCRCSTGG 136
 Db 330 ehheecdvcrcgstg 345

RESULT 7
 AAB24250
 ID AAB24250 standard; Protein; 345 AA.
 XX
 AC AAB24250;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human platelet-derived growth factor related protein LP8.
 XX
 KW Human; platelet derived growth factor related protein; LP8; VEGFh;
 KW vascular endothelial growth factor h; tissue regeneration; vulnery;
 KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO200059940-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US06427.
 XX
 PR 06-APR-1999; 99US-0127913.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Hammond LJ, Na S;
 XX
 DR WPI; 2000-664991/64.
 DR N-PSDB; AAC64426.
 XX
 XX Enhancing tissue growth and promoting wound healing by administering
 XX platelet-derived growth factor related protein, LP8 or its analog and
 XX treating atherosclerosis by administering LP8 antagonist -
 PS Claim 4; Page 63-64; 64pp; English.
 XX
 CC The present invention describes a method for enhancing tissue growth,
 CC promoting wound healing or stimulating smooth muscle growth by
 CC administering a platelet-derived growth factor (PDGF) related protein,
 CC designated LP8 or its analogue. Also described is a method of slowing
 CC the progress of atherosclerosis or treating atherosclerosis comprising
 CC the administration of an LP8 antagonist. The method is useful for
 CC enhancing tissue growth, promoting wound healing and stimulating smooth

CC muscle growth. Antagonists of LP8 are useful for treating
 CC atherosclerosis. The present sequence represents human LP8, which is
 CC also called VEGFh.
 XX
 XX Sequence 345 AA;

Query Match 100.0%; Score 754; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTVEVRLYSCTPRNFSVSIREELKRTDTI 60
 Db 210 ldledlyrptwqlgkafvgrksrvvdnlnteervlyscprnfsvsireelkrtdti 269
 QY 61 FWPGLLVKRCGNCACCLHNCQCVPKVKYHEVLQLRPKTGVRGLHKLSTLTDVAL 120
 Db 270 fwpgcllvkrcgncacclhncqcvpkvtkkyhevlqlrpkgtgvrghlksltdval 329
 QY 121 EHHEECDCVCRGSTGG 136
 Db 330 ehheecdvcrgstgg 345

RESULT 8
 AAB44322
 ID AAB44322 standard; Protein; 345 AA.
 XX
 AC AAB44322;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
 KW expressed sequence tag; detection; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US28565.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin DJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Sheiton IU, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2000-611443/58.
 DR

DR N-PSDB; AAC78582.

XX Novel PRO polypeptides and polynucleotides used in detection methods;
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX

PS Claim 12; Fig 207; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC the polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX Sequence 345 AA;

Query Match 100.0%; Score 754; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 4.7e-71;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTVEVRLYSCTPRNFSVSIREELKRTDTI 60
 Db 210 ldledlyrptwqlgkafvgrksrvvdnlnteervlyscprnfsvsireelkrtdti 269
 QY 61 FWPGLLVKRCGNCACCLHNCQCVPKVKYHEVLQLRPKTGVRGLHKLSTLTDVAL 120
 Db 270 fwpgcllvkrcgncacclhncqcvpkvtkkyhevlqlrpkgtgvrghlksltdval 329
 QY 121 EHHEECDCVCRGSTGG 136
 Db 330 ehheecdvcrgstgg 345

RESULT 9

AAB10633
 ID AAB10633 standard; Protein; 345 AA.

XX
 AC AAB10633;

XX
 DT 19-JAN-2001 (first entry)

XX
 DE Human RACE generated VEGF-X protein.

XX
 KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

XX WO200037641-A2.

XX
 PD 29-JUN-2000.

XX
 PF 21-DEC-1999; 99WO-US30503.

XX
 PR 22-DEC-1998; 98GB-0028377.

XX
 PR 18-MAR-1999; 99US-0124967.

XX
 PR 08-NOV-1999; 99US-0164131.

XX
 PA (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

XX Dhanaraj SN, Xu J;

```

XX WPI: 2000-442669/38.
DR N-PSDB; AAA71951.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 6; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-x
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the RACE generated human VEGF-X
CC protein described in the method of the invention.
XX
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 754; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTVEVRLYSCVTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTVEVRLYSCVTPRNFVSIREELKRTDTI 269
QY 61 FWPGLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRGLHKSITDVAL 120
DB 270 FWPGLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRGLHKSITDVAL 329
QY 121 EHHEEDCVCRGSTGG 136
DB 330 EHHEEDCVCRGSTGG 345
RESULT 10
AAB10634
ID AAB10634 standard; Protein; 345 AA.
XX
XX AAB10634;
XX
XX 19-JAN-2001 (first entry)
DE Human VEGF-X homologue protein.
DE
XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
XX Homo sapiens.
OS
XX WO200037641-A2.
PN
XX 29-JUN-2000.
PD
XX 21-DEC-1999; 99WO-US30503.
XX
XX 22-DEC-1998; 98GB-0028377.
PR

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PR 18-MAR-1999; 99US-0124967.
XX 08-NOV-1999; 99US-0164131.
XX
XX (JANC ) JANSSEN PHARM NV.
XX
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX
XX WPI: 2000-442669/38.
DR N-PSDB; AAA71952.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 7; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-x
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC homologue described in the method of the invention.
XX
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 754; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTVEVRLYSCVTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWQLGKAFVGRKSRVVDNLNLTVEVRLYSCVTPRNFVSIREELKRTDTI 269
QY 61 FWPGLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRGLHKSITDVAL 120
DB 270 FWPGLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRGLHKSITDVAL 329
QY 121 EHHEEDCVCRGSTGG 136
DB 330 EHHEEDCVCRGSTGG 345
RESULT 11
AAB10635
ID AAB10635 standard; Protein; 345 AA.
XX
XX AAB10635;
XX
XX 19-JAN-2001 (first entry)
DE Human VEGF-X protein #1 isolated from clones 4 and 7.
DE
XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
XX Homo sapiens.
OS
XX

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PN WO200037641-A2.
PD 29-JUN-2000.
XX 21-DEC-1999; 99WO-US30503.
XX 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX (JANC) JANSSEN PHARM NV.
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX WPI: 2000-442669/38.
DR N-PSDB; AAA71955.
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX Disclosure; Fig 9; 127pp; English.
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC isolated from clones 4 and 7 described in the method of the invention.
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 754; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDLEDLYRPTWQLLGKAFVGRKSRVVDNLNLTVEVRLYSCTPRNFSVSIREELKRTDTI 60
Db 210 LDLEDLYRPTWQLLGKAFVGRKSRVVDNLNLTVEVRLYSCTPRNFSVSIREELKRTDTI 269
Qy 61 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYHEVLQRLPKTGVRGLHKSILTDVAL 120
Db 270 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYHEVLQRLPKTGVRGLHKSILTDVAL 329
Qy 121 EHHCECDVCVRGSGTG 136
Db 330 ehheecdcvcrgstgg 345
RESULT 12
AAB10636
ID 'AAB10636 standard; Protein; 345 AA.
XX AAB10636;
AC AAB10636;
XX 19-JAN-2001 (first entry)
DT Human VEGF-X protein #2 isolated from clones 4 and 7.
XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX Homo sapiens.
OS WO200037641-A2.
PN 29-JUN-2000.
XX 21-DEC-1999; 99WO-US30503.
XX 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX (JANC) JANSSEN PHARM NV.
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX WPI: 2000-442669/38.
DR N-PSDB; AAA71955.
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX Claim.1; Fig 10; 127pp; English.
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC isolated from clones 4 and 7 described in the method of the invention.
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 754; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDLEDLYRPTWQLLGKAFVGRKSRVVDNLNLTVEVRLYSCTPRNFSVSIREELKRTDTI 60
Db 210 LDLEDLYRPTWQLLGKAFVGRKSRVVDNLNLTVEVRLYSCTPRNFSVSIREELKRTDTI 269
Qy 61 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYHEVLQRLPKTGVRGLHKSILTDVAL 120
Db 270 FWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYHEVLQRLPKTGVRGLHKSILTDVAL 329
Qy 121 EHHCECDVCVRGSGTG 136
Db 330 ehheecdcvcrgstgg 345
RESULT 13
AAB10644
ID 'AAB10644 standard; Protein; 345 AA.
XX AAB10644;
AC AAB10644;


```
XX 19-JAN-2001 (first entry)
XX Human VEGF-X protein #4.
DE VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
XX WO200037641-A2.
PN
XX 29-JUN-2000.
PD
XX 21-DEC-1999; 99WO-US30503.
PF
XX 22-DEC-1998; 98GB-0028377.
PR
XX 18-MAR-1999; 99US-0124967.
PR
XX 08-NOV-1999; 99US-0164131.
PR
XX (JANC ) JANSSEN PHARM NV.
PA
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
XX WPI: 2000-442669/38.
DR
XX N-PSDB; AAA71990.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 30B; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents a human VEGF-X protein
CC described in the method of the invention.
XX
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 754; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDLEDLYRPTWOLLGKAFVGRKSRVVDNLLTEVRLYSCPTPNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWOLLGKAFVGRKSRVVDNLLTEVRLYSCPTPNFVSIREELKRTDTI 269
QY 61 FWPGLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTVGRGLHSLTDVAL 120
DB 270 fwpqllvkrccgncacclhncnecqcvpskvtkkyhevlqlrpkgtvrglhksltdval 329
QY 121 EHHEEDCVCVRGSGTG 136
DB 330 ehheecdvcvrgstgg 345
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RESULT 14
AAB10650
ID AAB10650 standard; Protein; 345 AA.
AC AAB10650;
XX 19-JAN-2001 (first entry)
DE Human 990126vegX protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
XX WO200037641-A2.
PN
XX 29-JUN-2000.
PD
XX 21-DEC-1999; 99WO-US30503.
PF
XX 22-DEC-1998; 98GB-0028377.
PR
XX 18-MAR-1999; 99US-0124967.
PR
XX 08-NOV-1999; 99US-0164131.
PR
XX (JANC) JANSSEN PHARM NV.
PA
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
XX WPI: 2000-442669/38.
DR
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 11; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human 990126vegX protein
CC used to illustrate the method of the invention.
XX
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 754; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDLEDLYRPTWOLLGKAFVGRKSRVVDNLLTEVRLYSCPTPNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWOLLGKAFVGRKSRVVDNLLTEVRLYSCPTPNFVSIREELKRTDTI 269
QY 61 FWPGLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTVGRGLHSLTDVAL 120
DB 270 fwpqllvkrccgncacclhncnecqcvpskvtkkyhevlqlrpkgtvrglhksltdval 329
QY 121 EHHEEDCVCVRGSGTG 136
DB 330 ehheecdvcvrgstgg 345

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Db 270 fwpgccllvkrccgncacclhncncqcvpskvtkkyhevlqlrpkgtgvrghksltdval 329
Qy 121 EHHCECDCVCRGSTGG 136
Db 330 ehheecdcvcrgstgg 345

RESULT 15
AAB10651
ID AAB10651 standard; Protein; 345 AA.
AC AAB10651;
XX
DT 19-JAN-2001 (first entry)
DE Human VEGF-X protein #3.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW anticrheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
XX WO200037641-A2.
XX
XX 29-JUN-2000.
XX
XX 21-DEC-1999; 99WO-US30503.
XX
XX 22-DEC-1998; 98GB-0028377.
XX 18-MAR-1999; 99US-0124967.
XX 08-NOV-1999; 99US-0164131.
XX
XX (JANC ) JANSSEN PHARM NV.
XX
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
XX Dhanaraj SN, Xu J;
XX
XX WPI; 2000-442669/38.
XX
XX New vascular endothelial growth factor protein, useful for treating or
XX preventing diseases associated with inappropriate angiogenesis activity
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Claim 72; Fig 12; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
XX antidiabetic activity and acts as an angiogenesis and vascularization
XX regulator. An antisense molecule of the invention is useful for treating
XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX retinopathy by inhibiting angiogenic activity or inappropriate
XX vascularization including formation and proliferation of new blood
XX vessels, growth and development of tissues, tissue regeneration and organ
XX and tissue repair in a subject. The products of the invention are useful
XX for preparing medicaments for treating wounds such as dermal ulcers,
XX pressure sores, venous sores, diabetic ulcers and burns and to promote
XX skin graft growth, tissue repair, proliferation of new blood vessels,
XX tissue regeneration and organ repair by promoting angiogenic activity or
XX vascularization. This sequence represents the human VEGF-X protein
XX described in the method of the invention.
XX
XX Sequence 345 AA;
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Query Match 100.0%; Score 754; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LDLEDLYRPTWQLLGKAFVFGKRSRVVDNLLTTEVRLYSCTPRNFSVSIREELKRTDTI 60
Db 210 ldledlyrptwqllgkafvfgkrsvvdnlltteevrlyscprnfsvsireelkrtdti 269
Qy 61 FWPGCCLLVKRCGNCACCLHNCNECQCVPSCVTKKYHEVLQLRPKGTGVRGLHKSITDVAL 120
Db 270 fwpgccllvkrccgncacclhncncqcvpskvtkkyhevlqlrpkgtgvrghksltdval 329
Qy 121 EHHCECDCVCRGSTGG 136
Db 330 ehheecdcvcrgstgg 345
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Search completed: August 18, 2001, 01:49:50
Job time: 2231 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2001, 01:15:44 ; Search time 54.67 Seconds
(without alignments)
51.222 Million cell updates/sec

Title: US-09-457-066-2_COPY_210_345

Perfect score: 754

Sequence: 1 LDLEDLYRPTWQLGKAFV.....DVALEHHECDVCVCRSTGG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents-AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119.5	15.8	321	4	US-08-915-795-9
2	119.5	15.8	358	4	US-08-915-795-8
3	116	15.4	325	4	US-08-915-795-3
4	116	15.4	354	4	US-08-915-795-5
5	114.5	15.2	256	6	5175255-9
6	110	14.6	190	3	US-08-867-352-25
7	110	14.6	220	6	5175255-4
8	110	14.6	241	1	US-08-387-845-4
9	110	14.6	241	2	US-08-999-811-6
10	110	14.6	241	2	US-08-778-275-4
11	110	14.6	241	2	US-08-824-996-8
12	110	14.6	241	3	US-08-989-251-29
13	110	14.6	241	3	US-09-042-105-6
14	110	14.6	241	3	US-08-867-352-4
15	110	14.6	241	3	US-09-340-250-29
16	110	14.6	241	4	US-08-795-430-54
17	110	14.6	241	5	PCT-US96-09001-9
18	110	14.6	241	6	5194596-15
19	110	14.6	241	6	5219739-15
20	107	14.2	205	3	US-08-989-251-27
21	107	14.2	205	3	US-08-989-251-37
22	107	14.2	205	3	US-09-340-250-27
23	107	14.2	205	3	US-09-340-250-37
24	105.5	14.0	188	1	US-08-469-427A-11
25	105.5	14.0	188	2	US-08-609-443B-11
26	105.5	14.0	188	2	US-08-569-063C-11
27	105.5	14.0	188	4	US-08-795-430-57

28 105.5 14.0 207 2 US-08-609-443B-15
29 105.5 14.0 207 2 US-08-569-063C-15
30 105 13.9 109 1 US-08-094-079-2
31 105 13.9 109 1 US-08-094-079-3
32 105 13.9 109 2 US-08-804-953-3
33 105 13.9 109 3 US-08-691-794-4
34 105 13.9 109 5 PCT-US91-02766-18
35 105 13.9 109 5 PCT-US93-02612-1
36 105 13.9 109 6 5498600-3
37 105 13.9 119 2 US-08-257-494D-1
38 105 13.9 120 6 5428135-2
39 105 13.9 146 3 US-08-989-251-2
40 105 13.9 146 3 US-08-989-251-25
41 105 13.9 146 3 US-09-340-250-2
42 105 13.9 146 3 US-09-340-250-25
43 105 13.9 160 1 US-08-094-079-1
44 105 13.9 282 1 US-08-445-847A-1
45 104.5 13.9 109 3 US-08-691-794-3

ALIGNMENTS

RESULT 1
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match 15.8%; Score 119.5; DB 4; Length 321;
Best Local Similarity 33.3%; Pred. No. 2e-05;
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

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QY 29 LNLTEEVRLYSCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECQC 87
Db 99 LKVIDEEMORTQCSPRETCVEASELGKTTNTFFKPPCVNFRCGG---CC--NEEGVMC 153
QY 88 V---PSKVTYKHYEVLQRLPKTGVRGLKSLTDVALEHHEECDCVCRG 132
Db 154 MNTSTYSISKQLFEISV--PLTSV----PELVPVKIANHTGCKCLPTG 195

RESULT 2
US-08-915-795-8
; Sequence 8, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
; US-08-915-795-8

Query Match 15.8%; Score 119.5; DB 4; Length 358;
Best Local Similarity 33.3%; Pred. No. 2.3e-05;
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

QY 29 LNLTEEVRLYSCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECQC 87
Db 104 LKVIDEEMORTQCSPRETCVEASELGKTTNTFFKPPCVNFRCGG---CC--NEEGVMC 158
QY 88 V---PSKVTYKHYEVLQRLPKTGVRGLKSLTDVALEHHEECDCVCRG 132
Db 159 MNTSTYSISKQLFEISV--PLTSV----PELVPVKIANHTGCKCLPTG 200

RESULT 3
US-08-915-795-3
; Sequence 3, Application US/08915795
```

```
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-08-915-795-3

Query Match 15.4%; Score 116; DB 4; Length 325;
Best Local Similarity 28.3%; Pred. No. 4.9e-05;
Matches 43; Conservative 19; Mismatches 56; Indels 34; Gaps 8;

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Db 21 LEEELRITHSEDKWLKRLKLSFTSMDSRSASHSTRFAATFYDIETLKVIDEEMQRT 80
QY 40 SCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNEC-QCVPSKVTYKHY 97
Db 81 QCSPRETCVEASELGKSTNTFFKPPCVNFRCGG---CCNEESLICMNTSTYSISKQLF 137
QY 98 EVLQRLPKTGVRGLKSLTDVALEHHEECDCV 129
Db 138 EISV--PLTSV----PELVPVKIANHTGCKCL 163

RESULT 4
US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
;; STREET: 1200 G Street, NW, Suite 700
;; CITY: Washington
;; STATE: DC
;; COUNTRY: United States of America
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/915,795
;; FILING DATE:
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D.
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 1064/42983
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; TELEX: N/A
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 354 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; TISSUE TYPE: Human Lung
US-08-915-795-5

Query Match 15.4%; Score 116; DB 4; Length 354;
Best Local Similarity 28.3%; Pred. No. 5.4e-05;
Matches 43; Conservative 19; Mismatches 56; Indels 34; Gaps 8;

QY 3 LEDLYRPT-----WQL-----LGKAFVGRKSR-----VVDLNLLEEVRLY 39
DB 50 LEELLRIHSEDKMLRCLRLKLSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEMQRT 109
QY 40 SCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNEC-QCVPKSVTKKYH 97
DB 110 QCSPTCTVEASELKGKSTNFFKPCVNVFRCGG-----CCNEESLICMTSTYSISKOLF 166
QY 98 EVLQRPKGTGVRGLHKSLLTDVALEHHEECDCV 129
DB 167 EISV--PLTSV-----PELVPKVANHTGCKCL 192

RESULT 5
5175255-9
; Patent No. 5175255
; APPLICANT: Thomason, Arlen R.; Nicholson, Margery
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
; DERIVED FACTOR
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/25,344
; FILING DATE: 23-MAR-1987
; SEQ ID NO: 9:
; LENGTH: 256
5175255-9

Query Match 15.2%; Score 114.5; DB 6; Length 256;
Best Local Similarity 34.4%; Pred. No. 5.3e-05;
Matches 45; Conservative 9; Mismatches 36; Indels 41; Gaps 10;

QY 12 QLLGKAF-----VFGKSRVVD-LNLLTEEV--RLYCTPRNFVSIREELKRTDTIFWPG 64
DB 92 QYLSKVFNTNNLVFGTSDRVFEKLKLEEGISRLIDRTNANFLV-----WPP 138
QY 65 CLLVKRCGNCACCLHNCNECQCPKSVTKKYHEVLQLRP-----KTGV---RGLHKSLLTD 117
DB 139 CVEVQRCSG---CC--NNRNVCQRPTQV-----QLRPVQVRKIEIVKVKPFIRKAT- 184
QY 118 VALEHHEECDC 128
DB 185 VTLEDHLACKC 195
RESULT 6
US-08-867-352-25
; Sequence 25, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,847
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-867-352-25

Query Match 14.6%; Score 110; DB 3; Length 190;
Best Local Similarity 32.9%; Pred. No. 0.00012;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;
QY 72 DLEDLYRPTWQLLGKAFVFGKSRVVDLNLTT--EEVRLYCTPRN--FSVSIREELKRT 57
DB 72 ELESAR-----GRRS---LGLATAEPAMIAECKTRTEVEFEIS--RRLIDRT 114
QY 58 DTIF--WPGCLLVKRCGNCACCLHNCNECQCPKSVTKKYHEVLQLRP-----KTGV--- 108
DB 115 NANFLWPPCPEVQRCSG---CC--NNRNVCQRPTQV-----QLRPVQVRKIEIVRK 161
QY 109 RGLHKSLLTDVALEHHEECDC 128
DB 162 KPDKKAT-VTLEDHLACKC 180

RESULT 7
5175255-4
; Patent No. 5175255
; APPLICANT: Thomason, Arlen R.; Nicholson, Margery
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
; DERIVED GROWTH FACTOR
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/25,344
; FILING DATE: 23-MAR-1987
; SEQ ID NO: 4:
; LENGTH: 220
5175255-4


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; Patent No. 6017731
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,251
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5784-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-989-251-29

Query Match          14.6%; Score 110; DB 3: Length 241;
Best Local Similarity 32.9%; Pred. No. 0.00015;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps

Qy   2 DLEDYPTWQLLGKAFVFGKRGRVDNLNLT--EEVRLYSCTPRN--FSVSIREELKRT 57
      :||| |           ||| |       : | | | : | | | : | | : ||
Db   72 ELESAR-----GRRS-----LGSITIAEPAMIAECKTRTEVFPEIS-RRLIDRT 114

Qy   58 DTIF-WPGCLLVKRCGGNCACLLHNCQCVPKVKTKYHEVLQLRP-----KTGV--- 108
      : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db   115 NANFLWPPCVCVQRCSG---CC--NNRNVCQRPTQV-----QLRPVQVRKIEIVRK 161
      : | | | : | | | : | | | : | | | : | | | : | | | : | | | :

Qy   109 RGLHKSLTDVALEHHBECDC 128
      : | | | : | | | : | | | : | | | : | | | : | | | :
Db   162 KPIFKAT-VTLEDHLACK 180

RESULT 13
US-09-042-105-6
; Sequence 6, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-09-042-105-6

Query Match 14.6%; Score 110; DB 3; Length 241;
Best Local Similarity 32.9%; Pred. No. 0.00015;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWQLLGKAFVGRKSRVVDNLIT--EEVRLYSCTPRN--FSVSIREELKRT 57
Db 72 ELESAR-----GRRS-----LGSLTIAEPAMIAECKTRTEVFEIS--RRLDRT 114
QY 58 DTIF--WPGCLLVKRGNGCACCLHNCNECQVPSKVKYHEVLQLRP---KTGV--- 108
Db 115 NANFLVMPPCVEVORCSG---CC--NNRNVQCRPTQV-----QLRPVQVRKIEIVRK 161
QY 109 RGLHKSITDVALEHHEECDC 128
Db 162 KPIFKKAT-VTLEDHLACKC 180

RESULT 14
US-08-867-352-4
; Sequence 4, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,847
```

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; FILING DATE:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-867-352-4

Query Match 14.6%; Score 110; DB 3; Length 241;
Best Local Similarity 32.9%; Pred. No. 0.00015;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWQLLGKAFVGRKSRVVDNLIT--EEVRLYSCTPRN--FSVSIREELKRT 57
Db 72 ELESAR-----GRRS-----LGSLTIAEPAMIAECKTRTEVFEIS--RRLDRT 114
QY 58 DTIF--WPGCLLVKRGNGCACCLHNCNECQVPSKVKYHEVLQLRP---KTGV--- 108
Db 115 NANFLVMPPCVEVORCSG---CC--NNRNVQCRPTQV-----QLRPVQVRKIEIVRK 161
QY 109 RGLHKSITDVALEHHEECDC 128
Db 162 KPIFKKAT-VTLEDHLACKC 180

RESULT 15
US-09-340-250-29
; Sequence 29, Application US/09340250
; Patent No. 6083723
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,250
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,251
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5784-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-340-250-29

Query Match 14.6%; Score 110; DB 3; Length 241;
Best Local Similarity 32.9%; Pred. No. 0.00015;
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```
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;
Qy 2 DLEDLYRPTWQLLGKAFVGRKSRVVDLNLIT--EEVRLYSCTPRN--FSVSIREEELKRT 57
Db 72 ELESAR-----GRRS----LGSLLTIAEPAMIAECKTRTEVFEIS--RRLIDRT 114
Qy 58 DTIF--WPGCLLVKRCGGNCACCLHNCNECCQVPSKVKYHVEVLQLRP----KTGV--- 108
Db 115 NANFLWPPFCVEVORCSG---CC--NNRNVOCRPTQV-----QLRPQVQRKIEIVRK 161
Qy 109 RGLHKSLLTDVVALEHHEECDC 128
Db 162 KPIFKKAT-VTLEDHLACKC 180
```

Search completed: August 18, 2001, 01:50:57
Job time: 2113 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2001, 01:36:44 ; Search time 58.9 Seconds
(without alignments)
175.887 Million cell updates/sec

Title: US-09-457-066-2_COPY_210_345
Perfect score: 754
Sequence: 1 LDLEDLYRPTWQLLGKARVF.....DVALEHHECDVCVCRGSTGG 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.5	15.2	148	D49530	16K vascular endot
2	110	14.6	166	JN0248	platelet-derived g
3	110	14.6	198	JS0735	platelet-derived g
4	110	14.6	241	PFHUG2	platelet-derived g
5	108	14.3	200	I51551	platelet-derived g
6	108	14.3	215	S08220	platelet-derived g
7	108	14.3	226	I51550	platelet-derived g
8	107	14.2	245	TVCTSS	platelet-derived g
9	104.5	13.9	232	A41551	vascular endotheli
10	104	13.8	196	B28964	platelet-derived g
11	104	13.8	197	S25096	platelet-derived g
12	104	13.8	211	PFHUG1	platelet-derived g
13	104	13.8	226	TVMVSS	PDGF-related trans
14	102.5	13.6	133	B49530	vascular endotheli
15	102.5	13.6	190	S52130	vascular endotheli
16	102.5	13.6	196	A37359	platelet-derived g
17	102.5	13.6	196	A48951	platelet-derived g
18	102.5	13.6	419	S69207	vascular endotheli
19	101.5	13.5	120	A33787	vascular endotheli
20	101.5	13.5	146	S57956	ovine vascular end
21	101.5	13.5	198	B40080	vascular endotheli
22	97	12.9	180	JC4680	vascular endotheli
23	97	12.9	207	JC4679	vascular endotheli
24	96.5	12.8	190	A35987	glioma-derived vas
25	95.5	12.7	190	B44881	vascular endotheli
26	95.5	12.7	214	A44881	vascular endotheli
27	94	12.5	225	S25097	platelet-derived g
28	94	12.5	241	PFMSG8	platelet-derived g
29	88	11.7	271	A25669	PDGF-related trans

30 86 11.4 128 2 I51295 vascular endotheli
31 83.5 11.1 3020 2 A43932 mucin 2 precursor,
32 80 10.6 158 2 A56125 placental growth f
33 79.5 10.5 149 2 A41236 placental growth f
34 77.5 10.3 3672 2 T23433 hypothetical prote
35 77.5 10.3 3704 2 T37316 probable laminin a
36 77 10.2 1307 2 T21283 hypothetical prote
37 75.5 10.0 108 2 G84522 similar to glibbere
38 74.5 9.9 167 2 G96828 hypothetical prote
39 73.5 9.7 173 2 T21710 hypothetical prote
40 72.5 9.6 437 2 A75194 glycogen synthase
41 72 9.5 171 2 S57894 laminin - Hydra vu
42 71.5 9.5 1188 2 D86236 protein F14N23.5 l
43 71.5 9.5 1945 2 T13937 plexin A - fruit f
44 71.5 9.5 3712 2 S18253 laminin alpha-1 ch
45 71 9.4 60 2 JC2420 metallothionein -

ALIGNMENTS

RESULT 1

D49530

16K vascular endothelial growth factor homolog A2R - Orf virus

C:Species: Orf virus

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

C:Accession: D49530

R:Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.

J. Virol. 68, 84-92, 1994

A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o

A:Reference number: A49530; MUID:94076465

A:Contents: NZ7

A:Accession: D49530

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <LYT>

A:Cross-references: GB:S67522; NID:9456900; PIDN:AA829223.1; PID:9456902

A:Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIIP:141426)

Query Match 15.2%; Score 114.5; DB 2; Length 148;

Best Local Similarity 30.2%; Pred. No. 0.00047;

Matches 29; Conservative 19; Mismatches 43; Indels 5; Gaps 3;

Qy 41 CTPNFSVSIREL-KRTDTIEWPGCLLVKRGCGCACCLHNCNEQCQVPSVKYKHYEV 99

46 CAPRDTVVTLGGEYPESTNLQNPRTVTRCSG---CCNGDQICTAVETRTVTTSV 102

Qy 100 LQLRPKTGYR-GLHKSLTDVALEHHEECDCVCRGST 134

103 TGVSSSGTNSGVSTNLQRISVTEHTKDCIGRTT 138

RESULT 2

JN0248

platelet-derived growth factor chain A3 precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 27-Jun-1994

C:Accession: JN0248

R:Nakahara, K.; Nishimura, H.; Kuro-O, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazak

Biochem. Biophys. Res. Commun. 184, 811-818, 1992

A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vas

A:Reference number: JN0248; MUID:92246970

A:Accession: JN0248

A:Molecule type: mRNA

A:Residues: 1-166 <NAK>

C:Superfamily: platelet-derived growth factor

F:1-22/Domain: propeptide (fragment) #status predicted <PRO>

F:23-166/Product: platelet-derived growth factor A3 chain #status predicted <MAT>

Query Match 14.6%; Score 110; DB 2; Length 166;

Best Local Similarity 30.5%; Pred. No. 0.0014;

A:Residues: 'SLSL', 17-20, 'RQ', 22-241 <JOH>
A:Cross-references: GB:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562
R:Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Res. 23, 2815-2822, 1995
A:Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron
A:Reference number: S58382; MUID:95388493
A:Accession: S58383
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'MFINGL', 22-200 <DIR>
A:Cross-references: EMBL:X83705; NID:9951023; PIDN:CAA58679.1; PID:9951025
R:Cook, A.L.; Kirwin, P.M.; Craig, S.; Bawden, L.J.; Green, D.R.; Price, M.J.; Richards
Biochem. J. 281, 57-65, 1992
A:Title: Purification and analysis of proteinase-resistant mutants of recombinant platelet
A:Reference number: I38108; MUID:92117992
A:Accession: I38108
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'M', 82-241 <COO>
A:Cross-references: EMBL:X83966; NID:9311378; PIDN:CAA45383.1; PID:935377
A:Note: mutagenized recombinant sequence
C:Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal origin
C:Genetics:
A:Gene: GDB:PDGFB
A:Cross-references: GDB:120709; OMIM:190040
A:Map position: 22q12.3-22q13.1
A:Introns: 57/3; 94/1; 192/3; 241/1
C:Complex: homodimer; heterodimer (see PIR:PFHUG1)
C:Superfamily: platelet-derived growth factor
C:Keywords: growth factor; mitogen
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-81/Domain: amino-terminal propeptide #status predicted <PRO>
F:82-190/Product: platelet-derived growth factor chain B #status experimental <MAT>
F:159-163/Region: receptor binding #status predicted
F:191-241/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:97-141,130-178,134-180/Disulfide bonds: #status experimental
F:124/Disulfide bonds: interchain (to 133 in homodimeric form) #status experimental
F:124/Disulfide bonds: interchain (to chain A-132 in heterodimeric form) #status predicted
F:133/Disulfide bonds: interchain (to 124 in homodimeric form) #status experimental
F:133/Disulfide bonds: interchain (to chain A-124 in heterodimeric form) #status predicted

Query Match 14.6%; Score 110; DB 1; Length 241;
Best Local Similarity 32.9%; Pred. No. 0.002;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;
QY . 2 DLEDLYRPTWQLGKAFVGRKSRVVDNLTLT--EEVRLYSCTPRN--FSVSIREELKRT 57
Db 72 ELESAR-----GRRS-----IGSLTIAEPAMIAECKTTFEVEIS--RRLIDRT 114
QY 58 DTIF--WPGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHVEVLQLRP---KTGV--- 108
Db 115 NANFLWPPCPEVQRCSG---CC---NNRNVCQRTQV-----QLRPQVRKIEIVRK 161
QY 109 RGLHKSITDVALEHHEDCD 128
Db 162 KPIFKKAT-VTLEDHLACKC 180

RESULT 5
I51551
Platelet-derived growth factor A chain short form precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I51551
R:Mercola, M.; Melton, D.A.; Stiles, C.D.
Science 241, 1223-1225, 1988
A:Title: Platelet-derived growth factor A chain is maternally encoded in xenopus embryos
A:Reference number: I51550; MUID:88321676
A:Accession: I51551
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-200 <MER>

A:Cross-references: GB:M23238; NID:9214650; PIDN:AAA49928.1; PID:9214651
C:Superfamily: platelet-derived growth factor

Query Match 14.3%; Score 108; DB 2; Length 200;
Best Local Similarity 30.8%; Pred. No. 0.0027;
Matches 40; Conservative 15; Mismatches 43; Indels 32; Gaps 9;
QY 16 KAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSI--REELKRTDTIF--WPGCLLVKRCG 72
Db 82 KRSVPSSRRKRSV-----EEAVPAICKTRTVIIEIPRSQIDPITSANFLIWPCCVEVKRCT 135
QY 73 GNCACCLHNCNCCQVPSKVTKYH-----EVLQRPKTVGRGLHKSITDVALEHHE 124
Db 136 G---CC--NTSSVKQPSRI---HHRSVKAVKVEYVRKKPK-----LKEVL--VRLEHL 180
QY 125 ECDVCVCGST 134
Db 181 ECTCTANSNS 190

RESULT 6
S08220
Platelet-derived growth factor chain A precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C:Accession: S08220
R:Bejcek, B.E.; Li, D.Y.; Deuel, T.F.
Nucleic Acids Res. 18, 680, 1990
A:Title: Nucleotide sequence of a cDNA clone of Xenopus platelet-derived growth factor
A:Reference number: S08220; MUID:90175018
A:Accession: S08220
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-215 <BEJ>
A:Cross-references: EMBL:X17545; NID:964973; PIDN:CAA35583.1; PID:964974
C:Superfamily: platelet-derived growth factor
C:Keywords: alternative splicing; growth factor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-91/Domain: propeptide #status predicted <PRO>
F:92-215/Product: platelet-derived growth factor chain A #status predicted <MAT>

Query Match 14.3%; Score 108; DB 2; Length 215;
Best Local Similarity 30.8%; Pred. No. 0.0028;
Matches 40; Conservative 15; Mismatches 43; Indels 32; Gaps 9;
QY 16 KAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSI--REELKRTDTIF--WPGCLLVKRCG 72
Db 82 KRSVPSSRRKRSV-----EEAVPAICKTRTVIIEIPRSQIDPITSANFLIWPCCVEVKRCT 135
QY 73 GNCACCLHNCNCCQVPSKVTKYH-----EVLQRPKTVGRGLHKSITDVALEHHE 124
Db 136 G---CC--NTSSVKQPSRI---HHRSVKAVKVEYVRKKPK-----LKEVL--VRLEHL 180
QY 125 ECDVCVCGST 134
Db 181 ECTCTANSNS 190

RESULT 7
I51550
Platelet-derived growth factor A chain long form precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I51550
R:Mercola, M.; Melton, D.A.; Stiles, C.D.
Science 241, 1223-1225, 1988
A:Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embr
A:Reference number: I51550; MUID:88321676
A:Accession: I51550
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-226 <WER>
A:Cross-references: GB:M23237; NID:9214648; PIDN:AAA49927.1; PID:g214649
C:Superfamily: platelet-derived growth factor

Query Match 14.3%; Score 108; DB 2; Length 226;
Best Local Similarity 30.8%; Pred. No. 0.003;
Matches 40; Conservative 15; Mismatches 43; Indels 32; Gaps 9;

QY 16 KAFVFGKSRVVDNLNLTTEVRLYSCTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCG 72
Db KRSVPSSRRKRSV-----EEAVPAICKTRTVIIEIPRSQIDPTSNFLIWPVPCVEVKRCT 135
QY 73 GNCACCLHNCNCCQVPSVKTKYH-----EVLQRPKTVGVRGLHLSLTDALEHHE 124
Db KRSVPSSRRKRSV-----EEAVPAICKTRTVIIEIPRSQIDPTSNFLIWPVPCVEVKRCT 135
QY 125 ECDVCRCGST 134
Db KRSVPSSRRKRSV-----EEAVPAICKTRTVIIEIPRSQIDPTSNFLIWPVPCVEVKRCT 135
QY 161 ECTCTANSNS 190
Db KRSVPSSRRKRSV-----EEAVPAICKTRTVIIEIPRSQIDPTSNFLIWPVPCVEVKRCT 135

RESULT 8
TVCTSS
platelet-derived growth factor chain B precursor - cat
N:Alternate names: PDGF-related transforming protein
C:Species: Felis silvestris catus (domestic cat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Mar-1996
C:Accession: A26402
R:Van den Ouweland, A.M.W.; Van Groningen, J.J.M.; Schalken, J.A.; Van Neck, H.W.; Bloom
Nucleic Acids Res. 15, 959-970, 1987
A:Title: Genetic organization of the c-sis transcription unit.
A:Reference number: A26402; MUID:87146463
A:Accession: A26402
A:Molecule type: mRNA
A:Residues: 1-245 <VAN>
C:Genetics:
A:Gene: sis
C:Superfamily: platelet-derived growth factor
C:Keywords: glycoprotein; growth factor; platelet; proto-oncogene; transforming protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-81/Domain: propeptide #status predicted <PRO>
F:82-194/Product: platelet-derived growth factor chain B #status predicted <MAT>
F:163-167/Region: receptor binding #status predicted
F:63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 107; DB 1; Length 245;
Best Local Similarity 30.4%; Pred. No. 0.004;
Matches 42; Conservative 15; Mismatches 45; Indels 36; Gaps 10;

QY 2 DLEDLYRPTWQLGKAFVGRKS--RVVDNLNLTTEVRLYSCTPRN--FSVSTREELKRT 57
Db ELESLSR-----GRSLGEAGSPVAPAMIAEKTRETEVFS--RRIDRT 118
QY 58 DTIF--WPGCLLVKRCGNCACCLHNCNCCQVPSVKTKY-----HEVLQRPKTVGVRG 110
Db NANFLVWPVPCVEVKRSV-----CC--NNRVQCRPTQVQLVQVRKIEVTKRP----- 167
QY 111 LUKSLTDVALEHHEECDC 128
Db VFKKAT-VTLEDHLACKC 184

RESULT 9
A41551
vascular endothelial growth factor 206 precursor - human
N:Alternate names: vascular permeability factor
N:Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VEGF
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C:Accession: A41551; C41551; B41551; A40454; B40454; A40079; A40080; JQ1463; JQ1
R:Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.

Mol. Endocrinol. 5, 1806-1814, 1991
A:Title: The vascular endothelial growth factor family: identification of a fourth mo
A:Reference number: A41551; MUID:92168017
A:Accession: A41551
A:Molecule type: mRNA
A:Residues: 1-232 <HOU1>
A:Cross-references: GB:S85192; NID:9246155; PID:g246156
A:Accession: C41551
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 183-232 <HOU2>
A:Accession: B41551
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-141, 227-232 <HOU>
R:Rischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.;
J. Biol. Chem. 266, 11947-11954, 1991
A:Title: The human gene for vascular endothelial growth factor. Multiple protein form
A:Reference number: A40454; MUID:91268072
A:Accession: A40454
A:Molecule type: DNA
A:Residues: 1-165, 183-232 <TII>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976;
A:Accession: B40454
A:Molecule type: DNA
A:Residues: 1-140, 'N', 183-232 <TII2>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977;
A:Accession: C40454
A:Molecule type: DNA
A:Residues: 1-141, 227-232 <TII3>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978
R:Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.
Science 246, 1309-1312, 1989
A:Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A:Reference number: A40079; MUID:90069609
A:Accession: A40079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-165, 183-232 <KEC>
A:Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301
R:Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1308-1309, 1989
A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A:Reference number: A40080; MUID:90069608
A:Accession: A40080
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 183-232 <LEU>
A:Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971
R:Weindel, K.; Marne, D.; Welch, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A:Title: AIDS-associated kaposi's sarcoma cells in culture express vascular endotheli
A:Reference number: JQ1463; MUID:92231879
A:Accession: JQ1463
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 183-232 <WEI>
A:Cross-references: EMBL:X62568; NID:g37658; PIDN:CAAA4447.1; PID:g37659
A:Experimental source: AIDS-Kaposi's sarcoma cell
A:Accession: JQ1464
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 227-232 <WE2>
A:Experimental source: AIDS-Kaposi's sarcoma cell
R:Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.;
J. Biol. Chem. 264, 20017-20024, 1989
A:Title: Human vascular permeability factor. Isolation from U937 cells.
A:Reference number: A34492; MUID:90062112
A:Accession: A34492
A:Molecule type: protein
A:Residues: 27-36; 43-49, 'R', 72-76, 'Q', 78-81; 59-71 <CON>
C:Comments: The most common of several alternatively spliced forms is VEGF 165.
C:Genetics:
A:Gene: GDB:VEGF
A:Cross-references: GDB:132244; OMIM:192240

A;Map position: 6p21-6p12

C;Function:

A;Description: promotes fluid and protein leakage from blood vessels

C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro-

F;1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V2>

F;1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status predic

F;1-141,227-232/Product: vascular endothelial growth factor 121 precursor #status predic

F;1-26/Domain: signal sequence #status predicted <SIG>

F;101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 104.5; DB 2; Length 232;
Best Local Similarity 27.0%; Pred. No. 0.0067;
Matches 24; Conservative 21; Mismatches 33; Indels 11; Gaps 4;

QY 41 CTPRNFYSIREL-KRTDTIFWPGCLLVKRCGNCACLLHNCNECQCVPSPVKTKYHEV 99
| | | | | | | | | | | | | | | | | | | | | :
D B 52 CHPIETLVDFIPEYDEIEYIFPSCVPLMRCGG---CC--NDEGLECVPTESNITMQI 106
: : : : : : : : : : : : : : : : : : : : : :

QY 100 LQLRPKTGVRLHKSLTDVALEHHEDCD 128
: : : : : : : : : : : : : : : : : : : : : :

D b 107 MRKKPHQG-----QHIGENSFLQHNKEC 130
: : : : : : : : : : : : : : : : : : : : : :

RESULT 10

B28964 platelet-derived growth factor chain A precursor splice form.2 - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999

C;Accession: B28964; B42002; B28122

R;Bonthonron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988

A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, a

A;Reference number: A28964; MUID:88144463

A;Accession: B28964

A;Molecule type: DNA

A;Residues: 1-196 <BON>

A;Cross-references: GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987; GB:

R;Bonthonron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992

A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA t

A;Reference number: A42002; MUID:92307656

A;Accession: B42002

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 152-196 <BO2>

R;Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988

A;Title: Structural characterization of the human platelet-derived growth factor A-chain

A;Reference number: A28122; MUID:88174698

A;Accession: B28122

A;Molecule type: mRNA

A;Residues: 1-63, TRD, 67-196 <ROP>

A;Cross-references: GB:M20488

A;Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65 a

C;Comment: Exon 6 is spliced out of this variant splice form. For the major splice form

C;Genetics:

A;Gene: GDB:PDGFA

A;Cross-references: GDB:120266; OMIM:173430

A;Map position: 7p22-7p22

C;Superfamily: platelet-derived growth factor

C;Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet

Query Match 13.8%; Score 104; DB 2; Length 196;
Best Local Similarity 34.0%; Pred. No. 0.0064;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;

QY 41 CTPRNFYSVI-REELKRTDTIF-WPGCLLVKRCGGNCACLLHNCNECQCVPKVSKV---TK 94
| | | | | | | | | | | | | | | | | | | | | :
D b 96 CKTRIVIVEIPRSQVDPTGANFLWPCEVEVKRTGT---CC--NTSSVKQCPSRVHHHSV 150
: : : : : : : : : : : : : : : : : : : : : :

QY 95 KYHEVLQLRPKTGVRGLHKLSLTDALEHHHECDC 128

[illegible]

A:Residues: 152-211 <B02>
R:Betscholtz, C.; Johnson, A.; Heldin, C.H.; Westermark, B.; Lind, P.; Urdea, M.S.; Eddy
Nature 320, 695-699, 1986
A:Title: cDNA sequence and chromosomal localization of human platelet-derived growth fac
A:Reference number: A01379; MUID:86203630
A:Accession: A01379
A:Molecule type: mRNA
A:Residues: 1-211 <B01>
A:CROSS-references: GB:X03795; NID:g35365; PIDN:CAA27421.1; PID:g35366
A:Experimental source: clonal glioma cell line U-343 MGAC12.6, a tumor cell line
R:Hoppe, J.; Schumacher, L.; Eichner, W.; Welch, H.A.
FEBS Lett. 223, 243-246, 1987
A:Title: The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distantly
A:Reference number: S00173; MUID:88030061
A:Accession: S00173
A:Molecule type: mRNA
A:Residues: 1-193, 'DVR' <HOP>
A:CROSS-references: EMBL:X06374; NID:g35363; PIDN:CAA29677.1; PID:g35364
R:Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betscholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988
A:Title: Structural characterization of the human platelet-derived growth factor A-chain
A:Reference number: A28122; MUID:88174698
A:Accession: A28122
A:Molecule type: mRNA
A:Residues: 1-63, 'TRD', 67-211 <ROR>
A:CROSS-references: GB:M20488
A:Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65 a
C:Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal ori
C:Comment: A carboxyl-terminal propeptide may be removed from the precursor by proteoly
C:Genetics:
A:Gene: GDB:PDGFA
A:CROSS-references: GDB:I20266; OMIM:173430
A:Map position: 7p22-7p22
A:Introns: 21/3; 54/1; 89/1; 151/3; 194/1
C:Complex: homodimer; heterodimer (see PIR:PRHUG2)
C:Superfamily: platelet-derived growth factor
C:Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-86/Domain: propeptide #status predicted <PRO>
F:87-211/Product: platelet-derived growth factor chain A #status predicted <MAT>
F:158-162/Region: receptor binding #status predicted
F:96-140, 129-177, 133-179/Disulfide bonds: #status predicted
F:123/Disulfide bonds: interchain (to chain B-133 in heterodimeric form) #status predict
F:123/Disulfide bonds: interchain (to 132 in homodimeric form) #status predicted
F:132/Disulfide bonds: interchain (to chain B-124 in heterodimeric form) #status predict
F:132/Disulfide bonds: interchain (to 123 in homodimeric form) #status predicted
F:134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 104; DB 1; Length 211;
Best Local Similarity 34.0%; Pred. No. 0.0069;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;
QY 41 CTPRNFVSII-REELKRYDTIF--WPGCLLVKRCGNCACCLHNCNECQVPSKV---TK 94
DB 96 CKTRVVIETPRNSQVDPTSANFLIMPVCEVQRCTG---CC---NTSSVRKQPSRVHRSV 150
QY 95 KYHEVLQRLPKGTGVRGLHKSILTDVALEHHEECDC 128
DB 151 KVAKVEYVRKKPKLKEV-----QVRLEHLEAC 179
RESULT 13
TVMVSS
PDGF-related transforming protein (sis) - simian sarcoma virus
N:Alternate names: p28-sis
C:Species: simian sarcoma virus
C:Date: 23-Jul-1983 #sequence_revision 20-Sep-1984 #text_change 31-Oct-1997
C:Accession: A01381
R:Devare, S.G.; Reddy, E.P.; Law, J.D.; Robbins, K.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 80, 731-735, 1983
A:Title: Nucleotide sequence of the simian sarcoma virus genome: demonstration that its
A:Reference number: A03982; MUID:83144004

A:Accession: A01381
A:Molecule type: genomic RNA
A:Residues: 1-226 <DEV>
C:Genetics:
A:Gene: sis
C:Superfamily: platelet-derived growth factor
C:Keywords: growth factor; transforming protein
F:6-226/Domain: platelet-derived growth factor chain B similarity <PDG>
Query Match 13.8%; Score 104; DB 1; Length 226;
Best Local Similarity 33.3%; Pred. No. 0.0073;
Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;
QY 32 LTEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGNCACCLHNCNECQ 87
DB 73 VAEPAMIAECKTRTEVEFIS--RRLIDRTNANFLVMPVCEVQRCSG---CC--NNRNVC 126
QY 88 VPSKVTYKHYEVLQRLP-----KTGV---RGLHKSILTDVALEHHEECDC 128
DB 127 RPTGV-----QLRPVQVRKIEIVRKKPIFKKAT-VTLEDHLACKC 165
RESULT 14
B49530
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus
C:Species: Orf virus
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: B49530
R:Lyttille, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o
A:Reference number: A49530; MUID:94076465
A:Contents: NZ2
A:Accession: B49530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <LYT>
A:CROSS-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:I41420, NCBI:P:141425)
Query Match 13.6%; Score 102.5; DB 2; Length 133;
Best Local Similarity 30.5%; Pred. No. 0.0063;
Matches 32; Conservative 18; Mismatches 40; Indels 15; Gaps 6;
QY 33 TEEVRLYSCTPRNFSVSIRE---ELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQV 89
DB 28 SEVLKGSECKPRPIVVPVSETHPEL--TSQRFNPVPCVTLMRCGG---CC--NDESLECV 80
QY 90 SKVTYKHYEVLQRLPKGTGVRGLHKSILTDVALEHHEECDCVCRGST 134
DB 81 TEEVNTMELLG-ASGSGSNQMQR----LSFVEHKKDCRPRFTT 120
RESULT 15
S52130
vascular endothelial growth factor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: S52130
R:Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A:Title: Nucleotide sequence and expression of the porcine vascular endothelial growth
A:Reference number: S52130; MUID:95143284
A:Accession: S52130
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-190 <SHA>
A:CROSS-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

Query Match 13.6%; Score 102.5; DB 2; Length 190;
Best Local Similarity 27.0%; Pred. No. 0.0087;
Matches 24; Conservative 20; Mismatches 34; Indels 11; Gaps 4;
QY 41 CTPRNFSVSIREEL-KRTDIFWEGCLLVKRCGGNACCLHNCNECQCVPKVKYHEV 99
| | | | | : | | | | | : | | | | :
Db 51 CRPIETLVDFQEPDEIEYIFKPCVFLMRCGG--CC--NDEGLECVPTTEFNITMQI 105
| | | | | : | | | | | : | | | | :
QY 100 LQLRPKTGVRGLHKSLTDVALEHHECDC 128
: : : : | : : : | : : : |
Db 106 MRIKPHQG-----QHIGEMSFLOHMKCEC 129

Search completed: August 18, 2001, 01:52:09
Job time: 925 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2001, 01:49:54 ; Search time 33.78 Seconds
(without alignments)
137.914 Million cell updates/sec

Title: US-09-457-066-2_COPY_210_345

Perfect score: 754

Sequence: 1 LDLEDLYRPTWQLLGKAFV.....DVALEHHEECDCVCRGSTGG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.5	15.2	148	1	VEGH_OREN7
2	110	14.6	213	1	PDGA_RABIT
3	110	14.6	241	1	PDGB_HUMAN
4	108.5	14.4	164	1	VEGF_CAVPO
5	108	14.3	226	1	PDGA_XENLA
6	107	14.2	245	1	PDGB_FELCA
7	105.5	14.0	188	1	VEGB_HUMAN
8	104.5	13.9	215	1	VEGF_HUMAN
9	104	13.8	204	1	PDGA_RAT
10	104	13.8	211	1	PDGA_HUMAN
11	104	13.8	211	1	PDGA_MOUSE
12	104	13.8	226	1	TSIS_SMSAV
13	102.5	13.6	133	1	VEGH_OREN2
14	102.5	13.6	190	1	VEGF_PIG
15	102.5	13.6	419	1	VEGC_HUMAN
16	101.5	13.5	146	1	VEGF_SHEEP
17	101.5	13.5	190	1	VEGF_BOVIN
18	101.5	13.5	415	1	VEGC_MOUSE
19	97	12.9	188	1	VEGB_MOUSE
20	96.5	12.8	190	1	VEGF_RAT
21	95.5	12.7	214	1	VEGF_MOUSE
22	94	12.5	225	1	PDGB_RAT
23	94	12.5	241	1	PDGB_MOUSE
24	90	11.9	241	1	PDGB_SHEEP
25	88.5	11.7	216	1	VEGF_CHICK
26	84	11.1	158	1	PLGF_MOUSE
27	83.5	11.1	5179	1	MUC2_HUMAN
28	79.5	10.5	170	1	PLGF_HUMAN
29	77.5	10.3	3672	1	LML2_CAEEL
30	73	9.7	60	1	MT_CHAC
31	73	9.7	60	1	MT_PAGBE
32	73	9.7	60	1	MT_PARCR
33	72	9.5	60	1	MT_DICLA

34	72	9.5	171	1	LMB1_HYDAT	Q27262 hydra atten
35	71.5	9.5	3712	1	LMA_DROME	Q00174 drosophila
36	71	9.4	60	1	MT_DREMO	P52726 oreochromis
37	71	9.4	60	1	MT_ZOAVI	P52728 zoarces viv
38	71	9.4	82	1	MT2B_LYCES	Q40158 lycopersico
39	71	9.4	82	1	MAO2_RICPR	Q9zdf6 rickettsia
40	70.5	9.4	846	1	ITBX_DROME	P11584 drosophila
41	70	9.3	68	1	MT3_HORSE	P37360 equus cabal
42	70	9.3	68	1	MT3_PIG	P55944 sus scrofa
43	70	9.3	447	1	CLUS_RABIT	Q9xsc5 oryctolagus
44	69.5	9.2	445	1	CLUS_CANFA	P25473 canis faml
45	69	9.2	60	1	MT_LIZAU	O13257 liza aurata

ALIGNMENTS

```

RESULT 1
VEGH_OREN7
ID VEGH_OREN7 STANDARD; PRT; 148 AA.
AC P52585;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.
GN A2R.
OS Orf virus (strain NZ7) (OV NZ-7).
OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OX NCBI_TaxID=73495;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94076465; PubMed=8254780;
RA Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;
RT "Homologs of vascular endothelial growth factor are encoded by the
RT poxvirus orf virus.
RL J. Virol. 68:84-92(1994).
CC -!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; S67522; AAB29223.1;
CC HSSP; P15692; 1VPE.
CC InterPro: IPR000072;
CC Pfam; PF00341; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; FALSE_NEG.
CC PROSITE; PS50278; PDGF_2; 1.
CC Mitogen; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1
CC CHAIN ? 148
CC VASCULAR ENDOTHELIAL GROWTH FACTOR
CC HOMOLOG.
CC DISULFID 46 88
CC BY SIMILARITY.
CC DISULFID 77 130
CC BY SIMILARITY.
CC DISULFID 81 132
CC BY SIMILARITY.
CC DISULFID 71 71
CC INTERCHAIN (BY SIMILARITY).
CC DISULFID 80 80
CC INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 95 95
CC N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 148 AA; 16078 MW; F0E13BA104CC73F8 CRC64;

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Query Match 15.2%; Score 114.5; DB 1; Length 148;
Best Local Similarity 30.2%; Pred. No. 7.8e-05;
Matches 29; Conservative 19; Mismatches 43; Indels 5; Gaps 3;
Oy 41 CTPNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNACCLHNCNECCQVPSVKYKHEV 99

RN RP SEQUENCE FROM N.A.
 RA Burgess J., Odell C.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RN RP SEQUENCE OF 1-53 FROM N.A.
 RX MEDLINE-97141927; PubMed-8981877;
 RA Simon M.-P., Pedoutour F., Sirvent N., Grosgeorge J., Minoletti F.,
 Coindre J.-M., Terrier-Lacombe M.-J., Mandahl N., Craver R.D.,
 RA Blin N., Sozzi G., Turc-Carel C., O'Brien K.P., Kedra D.,
 RA Fransson I., Guilbaud C., Dumanaki J.P.;
 RT "Deregulation of the platelet-derived growth factor B-chain gene via
 fusion with collagen gene COL1A1 in dermatofibrosarcoma protuberans
 and giant-cell fibroblastoma";
 RL Nat. Genet. 15:95-98(1997).
 RN [9]
 RN RP SEQUENCE OF 26-241 FROM N.A.
 RX MEDLINE-86164981; PubMed-3456904;
 RA Weich H.A., Sebald W., Schairer H.U., Hoppe J.;
 RT "The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase
 mRNA which codes for the sequence of the PDGF-B chain";
 RL FEBS Lett. 198:344-348(1986).
 RN [10]
 RN RP SEQUENCE OF 153-200 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-84236121; PubMed-6325745;
 RA Johnson A., Heldin C.H., Wasteson A., Westermark B., Deuel T.F.,
 Huang J.S., Seeburg P.H., Gray A., Ullrich A., Scrae G.,
 RA Stroobant P., Waterfield M.D.;
 RT "The c-sis gene encodes a precursor of the B chain of
 platelet-derived growth factor";
 RL EMBO J. 3:921-928(1984).
 RN [11]
 RN RP SEQUENCE OF 82-110.
 RX MEDLINE-83197379; PubMed-6844921;
 RA Antoniadis H.N., Hunkapiller M.W.;
 RT "Human platelet-derived growth factor (PDGF): amino-terminal amino
 acid sequence";
 RL Science 220:963-965(1983).
 RN [12]
 RN RP SEQUENCE OF 82-112.
 RX MEDLINE-83244981; PubMed-6306471;
 RA Waterfield M.D., Scrae G.T., Whittle N., Stroobant P., Johnson A.,
 Wasteson A., Westermark B., Heldin C.H., Huang J.S., Deuel T.F.;
 RT "Platelet-derived growth factor is structurally related to the
 putative transforming protein p28sis of simian sarcoma virus";
 RL Nature 304:35-39(1983).
 RN [13]
 RN RP MUTAGENESIS, & IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING.
 RX MEDLINE-92097530; PubMed-1661670;
 RA Clements J.M., Bawden L.J., Bloxidge R.E., Catlin G., Cook A.L.,
 Craig S., Drummond A.H., Edwards R.M., Fallon A., Green D.R.,
 RA Hellewell P.G., Kirwin P.M., Nayee P.D., Richardson S.J., Brown D.,
 RA Chahwala S.B., Snarey M., Winslow D.;
 RT "Two PDGF-B chain residues, arginine 27 and isoleucine 30, mediate
 receptor binding and activation";
 RL EMBO J. 10:4113-4120(1991).
 RN [14]
 RN RP INTERCHAIN DISULFIDE BONDS.
 RX MEDLINE-92283833; PubMed-1317862;
 RA Andersson M., Oestman A., Baekstroem G., Hellman U.,
 RA George-Nascimento C., Westermark B., Heldin C.H.;
 RT "Assignment of interchain disulfide bonds in platelet-derived growth
 factor (PDGF) and evidence for agonist activity of monomeric PDGF";
 RL J. Biol. Chem. 267:11260-11266(1992).
 RN [15]
 RN RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE-93010987; PubMed-1396586;
 RA Oefner C., D'Arcy A., Winkler F.K., Eggmann B., Hosang M.;
 RT "Crystal structure of human platelet-derived growth factor BB";
 RL EMBO J. 11:3921-3926(1992).
 CC CC -I- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS

CC CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC CC -I- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
 AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
 TRANSFORMATION PROCESSES.
 CC CC -I- PHARMACEUTICAL: AVAILABLE UNDER THE NAME REGRANEX (ORTHO-MCNEIL).
 USED TO PROMOTE HEALING IN DIABETIC NEUROPATHIC FOOT ULCERS.
 CC CC -I- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
 PDGF RECEPTOR.
 CC CC -I- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC CC -I- DATABASE: NAME-R&D Systems' cytokine source book;
 WWW="http://www.rndsystems.com/cyt_cat/pdgm.html".
 CC CC -I- DATABASE: NAME-Regranex; NOTE-Clinical information on Regranex;
 WWW="http://www.regranex.com/".
 CC CC -----
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 CC CC -----
 DR EMBL; K01401; AAA60552.1;
 DR EMBL; K01918; AAA60552.1; JOINED.
 DR EMBL; J00121; AAA60552.1; JOINED.
 DR EMBL; K01398; AAA60552.1; JOINED.
 DR EMBL; K01399; AAA60552.1; JOINED.
 DR EMBL; K01400; AAA60552.1; JOINED.
 DR EMBL; X02811; CAA26579.1;
 DR EMBL; M12783; AAA60553.1;
 DR EMBL; X02744; CAA26524.1;
 DR EMBL; K01917; AAA98793.1;
 DR EMBL; K01913; AAA98793.1; JOINED.
 DR EMBL; K01914; AAA98793.1; JOINED.
 DR EMBL; K01915; AAA98793.1; JOINED.
 DR EMBL; K01916; AAA98793.1; JOINED.
 DR EMBL; X03702; CAA27333.1;
 DR EMBL; X81010; CAB02635.1;
 DR EMBL; X00561; CAA25228.1;
 DR EMBL; X00561; CAA25229.1;
 DR EMBL; X98706; CAA67262.1;
 DR PIR; A94276; PFHUG2.
 DR PDB; 1PDG; 31-JAN-94.
 DR MIM; 190040;
 DR InterPro; IPR000072;
 DR InterPro; IPR002400;
 DR Pfam; PF00341; PDGF; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS0278; PDGF_2; 1.
 KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal;
 KW Pharmaceutical; 3D-structure.
 FT SIGNAL 1 20
 FT PROPEP 21 81
 FT CHAIN 82 190
 FT PROPEP 191 241
 FT PROPEP 108 108
 FT SITE 111 111
 FT SITE 111 111
 FT DISULFID 97 141
 FT DISULFID 130 178
 FT DISULFID 134 180
 FT DISULFID 124 124
 FT DISULFID 133 133
 FT CONFLICT 21 21
 FT CONFLICT 101 101
 FT CONFLICT 105 105
 FT CONFLICT 107 107
 FT STRAND 90 91
 FT STRAND 94 94
 Query Match 14.6%; Score 110; DB 1; Length 241;
 Best Local Similarity 32.9%; Pred. No. 0.00036;

PLATELET-DERIVED GROWTH FACTOR, B CHAIN.

INVOLVED IN RECEPTOR BINDING.
INVOLVED IN RECEPTOR BINDING.INTERCHAIN.
INTERCHAIN.E -> R (IN REF. 3).
T -> E (IN REF. 11).
E -> C (IN REF. 11).
S -> C (IN REF. 11).Score 110; DB 1; Length 241;
Pred. No. 0.00036;

Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY	2	DLEDLRPTWQLLGKAPVFGKRSRVDNLLT---	EEVRLYSCTPRN---	FSVSIREELKRT	57
		:	:	:	:
Db	72	ELESRLA-----	GRRS-----	LGLSLTAEPAMIAECKTRTEVFEIS--	RRLIDRT 114
QY	58	DTIF--WPGCLLYKRCGGNCACCLHNCNECQCVSKVTKYHEVLQLRP----	KTGV----		108
		: :	: :	: :	: :
Db	115	NANFLVMPPCVEVQRCSG---CC--	NNRNVOCRPTQV-----	QLRPVQVRKIEIVRK	161
QY	109	RLHKSITDVALEHHHECDC	128		
		: :	: :	: :	: :
Db	162	KPIFKKAT--VTLEDHLACK	180		

RESULT	4
VEGF_CAVPO	
ID	VEGF_CAVPO STANDARD; PRT; 164 AA.
AC	P26617;
DT	01-AUG-1992 (Rel. 23, Created)
DT	01-AUG-1992 (Rel. 23, Last sequence update)
DE	01-OCT-1996 (Rel. 34, Last annotation update)
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY
DE	FACTOR) (VPF).
GN	VEGF.
OS	Cavia porcellus (Guinea pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX	NCBI_TaxID=10141;
[1]	
RN	SEQUENCE FROM N.A.
RP	
RS	Berse B.;
RL	Submitted (xxx-1992) to the EMBL/GenBank/DDBJ databases.
CC	- !- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC	CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC	PERMEABILITY.
CC	- !- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC	- !- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS
CC	TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC	SIMILARITY).
CC	- !- SIMILARITY: BELONGS TO THE PDGFR/VEGF FAMILY OF GROWTH FACTORS.

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CC or send an email to license@isb-sib.ch).

CC	EMBL; M84230; AAA37057.1; -. HSP; P15692; 2VGH. InterPro; IPR000072; -. Pfam; PF00341; PDGF_1. PROSITE; PS00249; PDGF_1; 1. DR PROSITE; PS0278; PDGF_2; 1. KW Mitogen; Growth factor; Glycoprotein. FT FT DISULFID 25 67 BY SIMILARITY. FT DISULFID 56 101 BY SIMILARITY. FT DISULFID 60 103 BY SIMILARITY. FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY). FT DISULFID 59 59 INTERCHAIN (BY SIMILARITY). FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL). SQ SEQUENCE 164 AA; 19330 MW; 9EB86A81A9D5DCA4 CRC64;
----	-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

Query Match	14.4%	Score 108.5;	DB 1;	Length 164;
Best Local Similarity	26.5%;	Pred. No. 0.00035;		
Matches 27;	Conservative 21;	Mismatches 37;	Indels 17;	Gaps 5;

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QY      34  EEVRLYS-----CTPRNFVSYSREEL-KRTDTLFWPGCLLVKRCGGNCACCLHNCNEQ  86
      |||:  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      12  EEVYFMDVYKRSYCRPTEMLVDLFOEYDPDIEYLFKSCVPLMRGG---CC--NDSELE  66

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Qy	87	CVPSKVT	KY	HEVLQ	LRPK	TGVR	GLH	KS	LT	DVA	LEH	HEE	CDC	128
		:		::::		:	:	:	:	:	:	:	:	
Db	67	CVPT	EENIT	QIM	RIK	PHQ	-----	QHIG	EMSF	LQHS	KCEC			103

RESULT						5
ID	PDGA_XENLA	STANDARD;	PRT;	226 AA.		
AC	PDGA_XENLA					
DT	01-JAN-1990	(Rel. 13, Created)				
DT	01-JAN-1990	(Rel. 13, Last sequence update)				
DT	01-OCT-2000	(Rel. 40, Last annotation update)				
DE	PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)					
DE	(PDGFA)					

DE {PDGRA}.
DS Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
ON NCBI_TaxID=8355;
RX [1].
RN SEQUENCE FROM N.A.
RP TISSUE=Oocyte;
RC MEDLINE=88321676; PubMed=3413486;
RX Marcola M., Melton D.A., Stiles C.D.;
RA "Platelet-derived growth factor A chain is maternally encoded in
RT xenopus embryos.";
RL Science 241:1223-1225(1988).

RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Oocyte;

RX MEDLINE=90175018; PubMed=2308861;

RA Bejcek B.E., LI D.Y., Deuel T.F.;
PM "Nucleotide sequence of a cDNA clone of vonnein related to vonnein"

RT growth factor A-chain";
RT Nucleotide sequence of a cDNA clone of xenopus platelet-derived

RL Nucleic Acids Res. 18:680-680(1990).

CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN

CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO

CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT RO

IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUNDS OF FETTERED SOULS AND LEAVE AN IMPRINT IN THE HEART

CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL

CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN

CC TRANSFORMATION PROCESSES:
CC - 1 - ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM /SUOEN HERE/ AND

CC : ALTERNATIVE PRODUCTS: Z ISOFORMS; A LONG FORM (SHOWN HERE) AND
CC : SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING THE LONG FO

CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL

CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO

CC PDGF RECEPTOR.

CC -!- SIMILARITY: BELONGS TO THE PDGE/VEGF FAMILY OF GROWTH FACTORS
CC -----

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22

DR EMBL; M23237; AAA49927.1; -.

DR EMBL; M23238; AAA49928.1; -
DR EMBL: Y17545: CAA35583.1: -

DR EMBL AT1545, CAC35563.1,
DR PIR: S08220: S08220.

DR HSSP; P01127; 1PDG.

DR InterPro; IPR000072; -.

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DR InterPro; IPR002400; -
DR Pfam; PF00341; DCCF; 1
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DR PLAM; PF00341; PDGF; I.
DR PRINTS: PR00438: GFCYSKNOT

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS50278; PDGF_2; 1.

KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing

KW	Signal.	
FT	SIGNAL.	1 22

17	EUNOTIC	1	22
17			22

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EMBL: X05112; CAA28758.1; ALT_SEQ.
PIR: A26402; TVCTSS.
HSP: P01127; IPDG.
InterPro: IPR000072;
InterPro: IPR002400;
Pfam: PF00341; PDGF_1.
PRINTS: PR00438; GRCYSKNOT.
PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS02078; PDGF_2; 1.
KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal.
FT SIGNAL 1 20
FT PROPEP 21 81
FT CHAIN 82 194
FT PROPEP 195 245
FT DISULFID 101 145
FT DISULFID 134 182
FT DISULFID 138 184
FT DISULFID 128 128
FT DISULFID 137 137
SQ SEQUENCE 245 AA; 27787 MW; E7715291D9837512 CRC64;

Query Match 14.2% Score 107; DB 1; Length 245;
Best Local Similarity 30.4%; Pred. No. 0.00074;
Matches 4; Conservative 15; Mismatches 45; Indels 36; Gaps 10;

QY 2 LDEDLYPTWLLGKAFVFGRS--RVVDLMLLTTEEVRLYSCTPRN--FSVSIREELKRT 57
: : : : : : : : : : : : : : : : : : : :
Db 72 ELESLS-----GRSLGEAGSPVAEPAMIAECKTRTEVEFS--RRLIDRT 118

QY 58 DTIF--WPGCLLVKRGCGNCACCLHNCEOCVSKYTKY----HEVLQLRPKTGVRG 110
: : : : : : : : : : : : : : : : : : : :
Db 119 NANELVMPPCPEVQRCSG---CC--NNRNVCREPTQGLRLVQVRKIEIVKRKP----- 167

QY 111 LHKSITDVALEHHEECDC 128
: : : : : : : : : : : : : : : : : : : :
Db 168 VFKKAT-VTLEDHLACK 184

RESULT 7
VEGB_HUMAN STANDARD; PRT; 188 AA.

AC P49765;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR).
GN VEGFB OR VRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=96197355; PubMed=8637916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V., Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson U.; "Vascular endothelial growth factor B, a novel growth factor for endothelial cells."; Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP MEDLINE=97077124; PubMed=8919691;
RA Grimond S., Lagercrantz J., Drinkwater C., Sillos G., Townson S., Pollock P., Gotley D., Carson E., Rakar S., Nordenskjoeld M., Ward L., Hayward N., Weber G.; "Cloning and characterization of a novel human gene related to vascular endothelial growth factor.";


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DR EMBL; M21571; -; NOT_ANNOTATED_CDS.
DR EMBL; X03795; CAA27421.1; -
DR EMBL; X06374; CAA29677.1; -
DR EMBL; M20498; AAA60045.1; JOINED.
DR EMBL; M20488; AAA60045.1; JOINED.
DR EMBL; M20489; AAA60045.1; JOINED.
DR EMBL; M20490; AAA60045.1; JOINED.
DR EMBL; M20491; AAA60045.1; JOINED.
DR EMBL; M20492; AAA60045.1; JOINED.
DR EMBL; M20493; AAA60045.1; JOINED.
DR EMBL; M19988; AAA60046.1; -
DR EMBL; M21571; AAA60046.1; JOINED.
DR EMBL; M19984; AAA60046.1; JOINED.
DR EMBL; M19985; AAA60046.1; JOINED.
DR EMBL; M19986; AAA60046.1; JOINED.
DR EMBL; M19987; AAA60046.1; JOINED.
DR EMBL; M19988; AAA60046.1; JOINED.
DR EMBL; M19989; AAA60047.1; -
DR EMBL; M21571; AAA60047.1; JOINED.
DR EMBL; M19984; AAA60047.1; JOINED.
DR EMBL; M19985; AAA60047.1; JOINED.
DR EMBL; M19986; AAA60047.1; JOINED.
DR EMBL; M19987; AAA60047.1; JOINED.
DR EMBL; A09204; CAA00830.1; -
DR EMBL; S62078; AAB26566.1; -
DR PIR; A28964; PFHUG1.
DR PIR; B28964; B28964.
DR HSSP; P01127; 1PDG.
DR MIM; I73430; -
DR InterPro; IPR000072; -
DR InterPro; IPR002400; -
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 20
FT PROPEP 21 86
FT CHAIN 87 211
FT SITE 158 162
FT DISULFID 96 140
FT DISULFID 129 177
FT DISULFID 133 179
FT DISULFID 123 123
FT DISULFID 132 132
FT CARBOHYD 134 134
FT VARSPIC 194 196
FT VARSPIC 197 211
FT CONFLICT 64 66
FT SEQUENCE 211 AA; 24043 MW; 48633DDE558EFA43 CRC64;

Query Match 13.88; Score 104; DB 1; Length 211;
Best Local Similarity 34.08; Pred. No. 0.0013;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;

QY 41 CTRNFTSVSI-REELKRTDIF--WPGCLLVKRCGGNCACCLHNCQCQVPSKV---TK 94
| : : : : : | : : : : | : : : : | : : : : |
Db 96 CKTRTVIYEIPRQVDFTSFANFLWPCVFEVKTG---CC--NTSSVKCQPSRVHRSV 150
| : : : : : | : : : : | : : : : | : : : : |
QY 95 KYHEVLQLRPKTGVRGLHLSLTDVALEHHEECDC 128
| : : : : : | : : : : | : : : : | : : : : |
Db 151 KVAKVEVVRKPKLKEV-----QVRLEHLECAC 179
| : : : : : | : : : : | : : : : | : : : : |

RESULT 11
ID PDGA_MOUSE STANDARD; PRT; 211 AA.
AC E20033;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)

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DE (PDGF-1).
GN PDGFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
RC STRAIN=BALB/C;
RX MEDLINE=94031105; PubMed=1340209;
RA Rorsman F., Betsholtz C.;
RT "Characterization of the mouse PDGF A-chain gene. Evolutionary
RT conservation of gene structure, nucleotide sequence and alternative
RT splicing.";
RL Growth Factors 6:303-313(1992).
RN [2]
RP SEQUENCE FROM N.A. (SHORT FORM).
RC STRAIN=F9;
RX MEDLINE=90169294; PubMed=2155144;
RA Mercola M., Wang C., Kelly J., Brownlee C., Jackson-Grusby L.,
RA Stiles C., Bowen-Pope D.;
RT "Selective expression of PDGF A and its receptor during early mouse
RT embryogenesis.";
RL Dev. Biol. 138:114-122(1990).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEALS THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC
DR EMBL; S66873; AAB28740.2; -
DR EMBL; S66868; AAB28740.2; JOINED.
DR EMBL; S66869; AAB28740.2; JOINED.
DR EMBL; S66870; AAB28740.2; JOINED.
DR EMBL; S66871; AAB28740.2; JOINED.
DR EMBL; S66872; AAB28740.2; JOINED.
DR EMBL; S66874; AAB28741.2; -
DR EMBL; S66868; AAB28741.2; JOINED.
DR EMBL; S66869; AAB28741.2; JOINED.
DR EMBL; S66870; AAB28741.2; JOINED.
DR EMBL; S66871; AAB28741.2; JOINED.
DR EMBL; S66872; AAB28741.2; JOINED.
DR EMBL; M29464; AAA39903.1; -
DR PIR; A37359; A37359.
DR HSSP; P01127; 1PDG.
DR MGD; MGI:97527; Pdga.
DR InterPro; IPR000072; -
DR InterPro; IPR002400; -
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 20
FT PROPEP 21 86
FT SEQUENCE 211 AA; 24043 MW; 48633DDE558EFA43 CRC64;

```

REMOVED BY PROTEOLYSIS.


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RESULT 14
ID VEGF_PIG STANDARD; PRT; 190 AA.
AC P49151;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95143284; PubMed=7841203;
RA Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
RT "Nucleotide sequence and expression of the porcine vascular
RT endothelial growth factor."
RL Biochim. Biophys. Acta 1260:235-238(1995).
CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL; X81380; CAA57143.1; -.
DR HSP; P15692; ZVGH.
DR InterPro; IPR000072; -.
DR Pfam; PF00341; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 26 POTENTIAL.
FT FT 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT FT DISULFID 51 93 BY SIMILARITY.
FT FT DISULFID 82 127 BY SIMILARITY.
FT FT DISULFID 86 129 BY SIMILARITY.
FT FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT FT CARBOHYD 100 100 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 190 AA; 22368 MW; 04D40B8D7913047F CRC64;

Query Match 13.6%; Score 102.5; DB 1; Length 190;
Best Local Similarity 27.0%; Pred. No. 0.0016;
Matches 24; Conservative 20; Mismatches 34; Indels 11; Gaps 4;

QY 41 CTPRNFVSIVREEL-KRTDTIFVGGCLLVKRGCGNCACCLHNCNECOCVPSKYTKYHEV 99
DB 51 CRPIETTLVDIFQEPDDEIYIFKPSVPLMRGCG---CC--NDBGLELCVPEFNTMQI 105
QY 100 LQRPKPTGVRGLKSLTDVALEHHECDC 128
DB 106 MRIKPHOG-----QHIGEMSFLOHKNKEC 129

RESULT 15

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FT REPEAT 275 298 1.
FT REPEAT 299 322 2.
FT REPEAT 323 346 3.
FT REPEAT 347 365 4 (PARTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 419 AA; 46883 MW; 9F598719DB3E014F CRC64;

Query Match 13.6%; Score 102.5; DB 1; Length 419;
Best Local Similarity 28.2%; Pred No. 0.0036;
Matches 31; Conservative 15; Mismatches 43; Indels 21; Gaps 6;

Qy 29 LNLTEEVRLYSCTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECQC 87
Db 119 LKSIDNEWKTCQMPREVCIDVGKEFGVATNFFKPPCVSVYRCGG---CC--NSEGLQC 173

Qy 88 V---PSKYTKKYHEV---LQLRPKTGVRGLHKS LTDVALEHHEECDCVCR 131
Db 174 MNTSTSYLSKTLFEITVPLSQGPKP-----VTISFANHITSCRCMSK 214

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Search completed: August 18, 2001, 01:54:44
Job time: 290 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2001, 01:48:14 ; Search time 98.1 Seconds
(without alignments)
183.420 Million cell updates/sec

Title: US-09-457-066-2_COPY_210_345

Perfect score: 754

Sequence: 1 LDLEDLPRTWQLLKARVF.....DVALEHHREDCVCRGSTGG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mnc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-unclassified:*
13: sp-vertebrate:*
14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	754	100.0	345	4	Q9UL22 homo sapien
2	754	100.0	345	4	Q9NRA1 homo sapien
3	697	92.4	345	11	Q9QY71 mus musculus
4	681	90.3	345	11	Q9JHV8 mus musculus
5	679	90.1	345	11	Q9EQX6 mus musculus
6	673	89.3	345	13	Q91946 rattus norv
7	346.5	46.0	370	11	Q9EQT1 rattus norv
8	344.5	45.7	370	4	Q9GZP0 homo sapien
9	121.5	16.1	326	11	O35251 rattus norv
10	119.5	15.8	358	11	P97946 mus musculus
11	117	15.5	148	13	O42571 xenopus lae
12	117	15.5	194	13	O42572 xenopus lae
13	116	15.4	354	4	O43915 homo sapien
14	110	14.6	185	4	Q15354 homo sapien
15	110	14.6	226	4	Q9UF23 homo sapien
16	107	14.2	210	6	Q29613 felis silve
17	105.5	14.0	207	4	Q16528 homo sapien
18	104.5	13.9	147	4	Q9UH58 homo sapien
19	104.5	13.9	171	4	Q9H1W8 homo sapien

Query Match 100.0% Score 754; DB 4; Length 345;

20	104.5	13.9	174	4	Q9UL23	Q9ul23 homo sapien
21	104.5	13.9	209	4	O60720	O60720 homo sapien
22	104.5	13.9	232	4	Q9H1W9	Q9h1w9 homo sapien
23	104.5	13.9	254	4	Q16889	Q16889 homo sapien
24	102.5	13.6	190	6	Q9XSF3	Q9xsf3 canis famil
25	102.5	13.6	190	6	Q9GL52	Q9gl52 sus scrofa
26	102.5	13.6	208	6	Q9XSF4	Q9xsf4 canis famil
27	102.5	13.6	214	6	Q9XSF5	Q9xsf5 canis famil
28	102.5	13.6	214	6	Q9MYV3	Q9myv3 canis famil
29	102	13.5	188	6	Q9XS48	Q9xs48 bos taurus
30	102	13.5	193	6	Q9XS49	Q9xs49 bos taurus
31	102	13.5	301	5	Q9WVP6	Q9wvp6 drosophila
32	101.5	13.5	118	6	Q9WZB1	Q9wzbl ovis aries
33	101.5	13.5	124	6	Q9CK00	Q9ck00 callithrix
34	101.5	13.5	190	6	O77643	O77643 ovis aries
35	101.5	13.5	418	13	O57352	O57352 coturnix co
36	101.5	13.5	420	6	Q9XS50	Q9xs50 bos taurus
37	100.5	13.3	144	13	O73822	O73822 brachydanio
38	100.5	13.3	188	13	O73682	O73682 brachydanio
39	100.5	13.3	190	11	Q9QX39	Q9qx39 spalax leuc
40	98	13.0	75	6	O18843	O18843 oryctolagus
41	98	13.0	78	6	Q9N1S2	Q9n1s2 capreolus c
42	98	13.0	123	6	Q9N1S1	Q9n1s1 capreolus c
43	98	13.0	211	13	Q9PUF7	Q9puf7 gallus gall
44	97.5	12.9	146	11	Q9QXG6	Q9qxg6 rattus norv
45	97.5	12.9	190	6	Q9GKR0	Q9gkr0 equus cabal

ALIGNMENTS

RESULT 1

Q9UL22
ID Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED GROWTH FACTOR).
GN HSCDGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Tsai Y.J., Lee R.K.K., Lin S.P.;
RT "Falloletin, a novel growth factor like gene identified in human uterus."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family."
RL FEBS Lett. 475:97-102(2000).
DR EMBL; AF091434; AAF00049.1; -
DR EMBL; AB033831; BAB03266.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR000859; -
DR Pfam; PF00341; PDGF; 1.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

```
Best Local Similarity 100.0%; Pred. No. 3.1e-75;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 269

QY 61 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 120
DB 270 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 329

QY 121 EHHECDVCVRGSGTG 136
DB 330 EHHECDVCVRGSGTG 345

RESULT 2
Q9NRAL ID Q9NRAL PRELIMINARY; PRT; 345 AA.
AC Q9NRAL;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Batscholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a novel protease-activated ligand for the PDGF alpha
RT receptor.";
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL; AF244813; AAF80597.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR000859; -
DR Pfam; PF00341; PDGF_1;
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 754; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.1e-75;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 269

QY 61 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 120
DB 270 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 329

QY 121 EHHECDVCVRGSGTG 136
DB 330 EHHECDVCVRGSGTG 345

RESULT 3
Q9QY71 ID Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FALLOTEIN.

Best Local Similarity 100.0%; Pred. No. 3.1e-75;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 269

QY 61 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 120
DB 270 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 329

QY 121 EHHECDVCVRGSGTG 136
DB 330 EHHECDVCVRGSGTG 345

RESULT 4
Q9JHV8 ID Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS-WEBSTER/NIH;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: Dynamic expression in embryonic tissues during
RT organogenesis.";
RL Mech. Dev. 0:0-0(2000).
DR EMBL; AF286725; AAF91483.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR000859; -
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 90.3%; Score 681; DB 11; Length 345;
Best Local Similarity 87.5%; Pred. No. 3.6e-67;
Matches 119; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 269
```

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA cloning of fallotein from mouse ovary.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF117608; AAF22516.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR000859; -
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match 92.4%; Score 697; DB 11; Length 345;
Best Local Similarity 89.0%; Pred. No. 6.2e-69;
Matches 121; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 269

QY 61 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 120
DB 270 FWPGLLVKRCGGNCACCLHNCNECCQVPSKVKYKHYEVLQRPKTGVRGLHKSLLTDVAL 329

QY 121 EHHECDVCVRGSGTG 136
DB 330 EHHECDVCVRGSGTG 345

RESULT 4
Q9JHV8 ID Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS-WEBSTER/NIH;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: Dynamic expression in embryonic tissues during
RT organogenesis.";
RL Mech. Dev. 0:0-0(2000).
DR EMBL; AF286725; AAF91483.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR000859; -
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 90.3%; Score 681; DB 11; Length 345;
Best Local Similarity 87.5%; Pred. No. 3.6e-67;
Matches 119; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 60
DB 210 LDLEDLYRPTWLLGKAFVFGKSRVVDLNLTEEVRLYSCPTPRNFVSIREELKRTDTI 269
```

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RL FBBS Lett. 475:97-102(2000).
DR EMBL; AB033829; BAB03265.1; -.
DR InterPro; IPR000072; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
DR SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 89.3%; Score 673; DB 13; Length 345;
Best Local Similarity 86.8%; Pred. No. 2,7e-66;
Matches 118; Conservative 11; Mismatches 7; Indels 0; Gaps

Qy 1 LDLEDLYRPTWQLLGKAFVGRKSRVVDLLNLTVEVRLYSCTPRNFSVSIREECLKRTDTI 60
Db 210 LDLEDLYRPTWQLLGKAYIHGRKSRVVDLLNLTVEVRLYSCTPRNFSVSIREECLKRTDTI 269

Qy -61 FWPCLLLVKRCGGNCACCLHNCNCQCPVKVKYKHYEVLQLRPKGVRLGHLKSLTDVAL 120
Db 270 FWPLCLLVKRCGGNCACCHQNCNECCQIPYKVKYKHYEVLQLRPKGVRLGHLKSLTDVPEL 329

Qy 121 EHHEECDVCVRGSTGG 136
Db 330 EHHEECDVCVKGNSEG 345

RESULT 7
Q9EQT1 PRELIMINARY; PRt; 370 AA.
ID Q9EQT1
AC Q9EQT1;
DT 01-MAR-2001 (TremblRel. 16, Created)

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UI-MAR-2001 (TREMBLrel. 16, Last annotation update)	
SPINAL-CORD DERIVED GROWTH FACTOR-B.	
RSCDGF-B.	
Rattus norvegicus (Rat).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
NCBI_TaxID=10116;	
{1}	
SEQUENCE FROM N.A.	
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;	
"Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to	
SCDF/PDGF-C/fallotenein.";	
Biochem. Biophys. Res. Commun. 0:0-0(2000).	
EMBL; AB052170; BAB18920.1; -.	
SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;	

Query Match	46.0%; Score 346.5; DB 11; Length 370;
Best Local Similarity	50.0%; Pred. No. 3.3e-30;
Matches	66; Conservative 23; Mismatches 38; Indels 5; Gaps
Qy	--2 DLEDYRTWOLLGKARVFGKRSKVVDLNLLETVRLYSCTPRNFVSIREELKRDTTIF 61 : : : : :: :: :
Db	235 DLENLYMDTPRYGRGSY-HERKSK-VDLDRDNDVKRYSCTPRNHSVNLRRELKLTNAV 292 : : : : :
Qy	62 WPGCLLVKRCGGNCACCLHNCNEQCQVPSKYTKYHEVLQLRP---KTGVRGLHKSLTDV 118 : : : : : :
Db	293 FPRCLLVQRCGNGCGGTLANWKSCSSSGKTVRKYHEVLKFEPGHFKRRGAKNNALVDI 352 : : : : :
Qy	119 ALEHHEECDCVC 130 : :
Db	353 QLDHHERCDCIC 364 : :
RESULT	8
Q9GZP0	
ID	Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC	Q9GZP0;
OT	01-MAR-2001 (TREMBLrel. 16. Created)


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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036).
GN HSCDGF-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Ui-Tel K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
RT SCDGF/PDGF-C/fallotoin.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=AORTA;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033832; BAB18903.1;
DR EMBL; AF113216; AAG39287.1;
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;

Query Match 45.7%; Score 344.5; DB 4; Length 370;
Best Local Similarity 50.0%; Pred. No. 5.4e-30;
Matches 66; Conservative 21; Mismatches 40; Indels 5; Gaps 3;

QY 2 DLEDYRTWOLLKAFVFGKRSRVVDNLNLTVEVRLYSCPTPRNFSVSIREELKRTDTIF 61
DB 235 DLENYLTPRYRGSY-HDRKSK-VLDRLNDADKRYSCPTPRNFSVNIRELKLANVVF 292
QY 62 WPGCLLVKRCGNCACCLHNCNECOCVSKYTKYHEVLQLRP---KTGVRGLHKSITDV 118
DB 293 FPRCLLVORCGNCGCGVNWRSCTNCGTKVKYHEVLQFEPGHIKRRGRKTMALVDI 352
QY 119 ALEHHEECDCVC 130
DB 353 QLDHHERCDCIC 364

RESULT 9
O35251 ID O35251 PRELIMINARY; PRT; 326 AA.
AC O35251;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR D.
GN VEGF-D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY;
RX MEDLINE=97349118; PubMed=9205122;
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
DR EMBL; AF014827; AAB66557.1;
DR HSSP; P15692; IVPF.
DR InterPro; IPR000072;
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629;
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 358 AA; 40908 MW; 6636B17FBF07037C CRC64;

Query Match 15.8%; Score 119.5; DB 11; Length 358;
Best Local Similarity 33.3%; Pred. No. 3.6e-05;
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

QY 29 LNLTEVRLYSCPTPRNFSVSIREEL-KRDTTFWPCGLLVKRCGNCACCLHNCNECOC 87
DB 104 LKVIDEWMQRTQCPRETCEVASSELGKTNTFFKPCVNVFRCGG---CC--NEESVMC 158
QY 88 V---PSKVTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCVRG 132
DB 159 MNTSTSYISKQLFEISV--PLTSV----PELVVPVKIANHTGCKCLPTG 200

RESULT 11
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SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;

Query Match 16.1%; Score 121.5; DB 11; Length 326;
Best Local Similarity 33.3%; Pred. No. 2e-05;
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

QY 29 LNLTEVRLYSCPTPRNFSVSIREEL-KRDTTFWPCGLLVKRCGNCACCLHNCNECOC 87
DB 104 LKVIDEWMQRTQCPRETCEVASSELGKTNTFFKPCVNVFRCGG---CC--NEESVMC 158
QY 88 V---PSKVTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCVRG 132
DB 159 MNTSTSYISKQLFEISV--PLTSV----PELVVPVKIANHTGCKCLPTG 200

RESULT 10
P97946 ID P97946 PRELIMINARY; PRT; 358 AA.
AC P97946;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR D (C-FOS INDUCED GROWTH FACTOR).
GN VEGF-D OR FIGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=97030254; PubMed=8876195;
RA Ordanini M., Marconini L., Ferruzzi R., Oliviero S.;
RT "Identification of a c-fos-induced gene that is related to the
RT platelet-derived growth factor/vascular endothelial growth factor
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:11675-11675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=97349118; PubMed=9205122;
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
DR EMBL; X9572; CAA67892.1;
DR HSSP; P15692; IVPF.
DR MGD; MGI:108037; Figf.
DR InterPro; IPR000072;
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629;
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 358 AA; 40908 MW; 6636B17FBF07037C CRC64;

Query Match 15.8%; Score 119.5; DB 11; Length 358;
Best Local Similarity 33.3%; Pred. No. 3.6e-05;
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

QY 29 LNLTEVRLYSCPTPRNFSVSIREEL-KRDTTFWPCGLLVKRCGNCACCLHNCNECOC 87
DB 104 LKVIDEWMQRTQCPRETCEVASSELGKTNTFFKPCVNVFRCGG---CC--NEESVMC 158
QY 88 V---PSKVTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCVRG 132
DB 159 MNTSTSYISKQLFEISV--PLTSV----PELVVPVKIANHTGCKCLPTG 200

RESULT 11
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O42571
ID O42571 PRELIMINARY; PRT; 148 AA.
AC O42571;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 122.
GN VEGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008593; AAB63679.1;
DR HSSP; P15692; 1VPP.
DR InterPro; IPR000072;
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;

Query Match 15.5%; Score 117; DB 13; Length 148;
Best Local Similarity 26.0%; Pred. No. 2.7e-05;
Matches 34; Conservative 27; Mismatches 46; Indels 24; Gaps 7;

O42571
ID O42571 PRELIMINARY; PRT; 194 AA.
AC O42572;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 196.
GN VEGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008594; AAB63680.1;
DR HSSP; P15692; 1VGH.
DR InterPro; IPR000072;
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 194 AA; 22672 MW; 85D7BEC7CEFEFF17E CRC64;

O42571
ID O42571 PRELIMINARY; PRT; 354 AA.
AC O43915;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GROWTH FACTOR FIGF.
GN FIGF OR VEGF-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=97349118; PubMed=9205122;
RX Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118549; PubMed=9435229;
RX Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RX Alitalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
DR EMBL; Y12864; CAA73371.1;
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.
DR EMBL; Y12869; CAA73371.1; JOINED.
DR EMBL; Y12870; CAA73371.1; JOINED.
DR EMBL; D89630; BAA24264.1;
DR EMBL; AJ000185; CAA03942.1;
DR EMBL; Y12863; CAA73370.1;
DR HSSP; P15692; 1VPP.
DR InterPro; IPR000072;
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 354 AA; 40444 MW; 2048D769D735173E CRC64;
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Query Match 15.4%; Score 116; DB 4; Length 354;
Best Local Similarity 28.3%; Pred. No. 8.7e-05;
Matches 43; Conservative 19; Mismatches 56; Indels 34; Gaps 8;

QY 3 LEDLYRPT---WOL-----LQKAFVGRKSR-----VVDLNLITTEVRVLY 39
DB 50 LEELLRIHSEDMKLRCLRKSTMSDRSASHRSTFAATFYDITLKVIDEWQRT 109
QY 40 SCTPNFNSIREEEL-KRDTIFWPGCLLVKRCGGNCACCLHNCNEC-QCVPSKVTKKYH 97
DB 110 QCSPRETCVEASELGKSTNTEFKPCVNVFRCGG---CCNEESLICMTSTSYISKOLF 166
QY 98 EYLQLRPKTGVRLHKSLTDVALEHHEECDCV 129
DB 167 EISV--PLTSV----PELVPVKVANHTGCKCL 192

RESULT 14
Q15354 PRELIMINARY; PRT; 185 AA.
AC Q15354;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE C-SIS PROTO-ONCOGENE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CHORIOCARCINOMA;
RX MEDLINE=95388493; PubMed=7659502;
RA Dirks R.P.H., Onnekink C., Jansen H.J., de Jong A., Bloemers H.P.J.;
RT "A novel human c-sis mRNA species is transcribed from a promoter in c-
RT sis intron 1 and contains the code for an alternative PDGF B-like
RT protein.";
RL Nucleic Acids Res. 23:2815-2822(1995).
DR EMBL; X83705; CAA58679.1; -
DR HSP; P01127; IPDG.
DR InterPro; IPR000072; -
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
FT NON_TER 185
SQ SEQUENCE 185 AA; 20774 MW; A2BCS85F88DFEE59 CRC64;

Query Match 14.6%; Score 110; DB 4; Length 185;
Best Local Similarity 32.9%; Pred. No. 0.0002;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWLLGKAFVGRKSRVVDLNLIT--EEVRLYSCTPRN--FSVSIREELKRT 57
DB 57 ELESAR-----GRRS-----LGSLTIAEPAMIAECKTRTEVFEIS--RRLIDRT 99
QY 58 DTIF--WPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV--- 108
DB 100 NANFLVWPCCVEVQRCSG---CC--NNRNVCQRTQV-----QLRPVQVRKIEIVRK 146
QY 109 RGLHKSITDVALEHHEECDC 128
DB 147 KPIFKKAT-VTLEDHLACKC 165

RESULT 15
Q9UF23 PRELIMINARY; PRT; 226 AA.
AC Q9UF23;
DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CN10C3.1 (PLATELET-DERIVED GROWTH FACTOR BETA POLYPEPTIDE (SIMIAN
DE SARCOMA VIRAL (V-SIS) ONCOGENE HOMOLOG) (ISOFORM 2)).
GN PDGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Burgess J.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81010; CAB62507.1; -
DR HSP; P01127; IPDG.
DR InterPro; IPR000072; -
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 226 AA; 25502 MW; 523AC7394E29C0D5 CRC64;

Query Match 14.6%; Score 110; DB 4; Length 226;
Best Local Similarity 32.9%; Pred. No. 0.00025;
Matches 46; Conservative 13; Mismatches 37; Indels 44; Gaps 12;

QY 2 DLEDLYRPTWLLGKAFVGRKSRVVDLNLIT--EEVRLYSCTPRN--FSVSIREELKRT 57
DB 57 ELESAR-----GRRS-----LGSLTIAEPAMIAECKTRTEVFEIS--RRLIDRT 99
QY 58 DTIF--WPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV--- 108
DB 100 NANFLVWPCCVEVQRCSG---CC--NNRNVCQRTQV-----QLRPVQVRKIEIVRK 146
QY 109 RGLHKSITDVALEHHEECDC 128
DB 147 KPIFKKAT-VTLEDHLACKC 165

Search completed: August 18, 2001, 01:54:00
Job time: 346 sec

OM of: US-09-457-066-2_COPY_210_345 to: GenEmbl.* Out_format : pfs

Date: Aug 18, 2001 3:47 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame-p2n.model -DEV=xlp
-O=/gen2.1/USPTO_spool/US09457066/runat_17082001_083144_25088/app_query.fasta_1.207
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-MINMATCH=0.100 -LOOPCL=0.000 -LOAPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -EGAPOP=6.000
-EGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODEL=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09457066.@CGNL_1.4592 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-457-066-2_COPY_210_345

Query length: 136

Database: GenEmbl.*

Database sequences: 1344157

Database length: -856060004

Search time (sec): 1473.660000

score_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
gb_pat1:AX027935	+ 754.00	1414.46	1.5e-70	1035	AX027935 Sequence 3 from Patent
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LOCUS AX027935
DEFINITION Sequence 3 from Patent W00037641.
ACCESSION AX027935
VERSION AX027935.1 GI:10188752
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE Vascular endothelial growth factor-x
JOURNAL Patent: WO 0037641-A 3 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSTENA JOHANNA HUBER (BE) ;
JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
SRIDEVI NAIDU (US)

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VERSION AX028032.1 GI:10188844
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Von,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE Vascular endothelial growth factor-x
JOURNAL Patent: WO 0037641-A 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE); DIJKMANS JOSIENA JOHANNA HUBER (BE);
JANSSEN PHARMACEUTICA NV (BE); SPRENGEL JORG JURGEN (BE); YON
JEFFREY ROLAND (BE); XU JEAN (US); GOSIEWSKA ANNA (US); DHANARAJ
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DEFINITION Sequence 32 from Patent WO0066736.
ACCESSION AX044518
VERSION AX044518.1 GI:11343373
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gilbert,T., Hart,C.E., Shepard,P.O. and Gilbertson,D.G.
TITLE Growth factor homolog zvegfa
JOURNAL Patent: WO 0066736-A 32-09-NOV-2000;
ZymoGenetics, Inc. (US)
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 DEFINITION Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor, complete cds.
 ACCESSION AB033831
 VERSION AB033831.1 GI:9392293
 KEYWORDS spinal cord-derived growth factor; scdGF gene.
 SOURCE Homo sapiens embryo brain cDNA to mRNA.
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (sites)
 Hamada,T., Ui-Tei,K. and Miyata,Y.
 A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family(1)
 FEBS Lett. 475 (2), 97-102 (2000)
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 2 (bases 1 to 1817)
 Hamada,T., Ui-Tei,K. and Miyata,Y.
 Direct Submission
 Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases.
 Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan
 (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

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 DEFINITION Homo sapiens platelet-derived growth factor C mRNA, complete cds.
 ACCESSION AF244813
 VERSION AF244813.1 GI:8886883
 KEYWORDS
 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2152)
 Li,X., Ponten,A., Aase,K., Karlsson,L., Abramsson,A., Utela,M., Backstrom,G., Hellstrom,M., Bostrom,H., Li,H., Soriano,P., Belsholtz,C., Heldin,C.-H., Allitalo,K., Ostman,A. and Eriksson,U.
 PDGF-C is a novel protease-activated ligand for the PDGF alpha receptor
 Nat. Cell Biol. (2000) In press
 2 (bases 1 to 2152)
 Eriksson,U., Aase,K., Li,X. and Ponten,A.
 Direct Submission
 Submitted (14-MAR-2000) Ludwig Institute for Cancer Research, Nobels vag 3 P.O.Box 240, Stockholm S-171 77, Sweden
 Location/Qualifiers
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LOCUS AX047650
DEFINITION Sequence 9 from Patent WO0070050.

ACCESSION AX047650
VERSION AX047650.1 GI:11876693
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2849)
AUTHORS Baker,K.P., Chen,J., Ferrara,N., Fong,S., Goddard,A., Gurney,A.L., Hillan,K.J., Kuo,S.S., Tumas,D. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related diseases
JOURNAL Patent: WO 0070050-A 9 23-NOV-2000;
Genentech, Inc. (US)
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DEFINITION Homo sapiens secretory growth factor-like protein fallotein mRNA,
complete cds.
ACCESSION  AF091434
VERSION     AF091434.1  GI:6002592
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3007)
AUTHORS     Tsai,Y.-J., Lee,R.K., Lin,S. and Chen,Y.
TITLE       Identification of a novel platelet-derived growth factor-like gene,
fallotein, in the human reproductive tract
JOURNAL     Biochim. Biophys. Acta 1492 (1), 196-202 (2000)
MEDLINE     20461776
REFERENCE   2 (bases 1 to 3007)
AUTHORS     Tsai,Y.-J., Lee,R.K.K. and Lin,S.P.
TITLE       Direct Submission
JOURNAL     Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial
Hospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan
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LOCUS AF117608 2692 bp mRNA ROD 02-JAN-2000
DEFINITION Mus musculus fallotein mRNA, complete cds.

ACCESSION AF117608

VERSION AF117608.1 GI:6652867

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 2692)

AUTHORS Tsai,Y.-J., Lee,R.K.-K., Chen,Y.-H., Lin,S.-P. and Cheng,W.T.-K.

TITLE CDNA cloning of fallotein from mouse ovary

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2692)

AUTHORS Tsai,Y.-J., Lee,R.K.-K., Chen,Y.-H., Lin,S.-P. and Cheng,W.T.-K.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-1999) Medical Research, Mackay Memorial Hospital,

45 Min Sheng Road, Tamshui, Taipei 25115, Taiwan

FEATURES Location/Qualifiers

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DEFINITION Sequence 34 from Patent WO0066736.
ACCESSION AX044520
VERSION AX044520.1 GI:11343375
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 3571)
AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.
TITLE Growth factor homolog zveg14
JOURNAL Patent: WO 0066736-A 34 03-NOV-2000;
ZymoGenetics, Inc. (US)
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DEFINITION Mus musculus platelet-derived growth factor C (pdgfc) mRNA,
complete cds.
ACCESSION AF286725
VERSION AF286725.1 GI:9652343
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 1038)
AUTHORS Ding,H., Wu,X., Kim,I., Tam,P.P., Koh,G.Y. and Nagy,A.
TITLE The mouse pdgfc gene: dynamic expression in embryonic tissues
during organogenesis
JOURNAL Mech. Dev. 96 (2), 209-213 (2000)
MEDLINE 20417814
REFERENCE 2 (bases 1 to 1038)
AUTHORS Ding,H., Wu,X., Tam,P.P.L. and Nagy,A.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2000) Samuel Lunenfeld Research Institute, Mount
Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
Canada
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DEFINITION Rattus norvegicus rScd3gf mRNA for spinal cord-derived growth
factor, complete cds.
ACCESSION  AB033830
VERSION    AB033830.1 GI:11994799
KEYWORDS   spinal cord-derived growth factor; SCDGF.
SOURCE     Rattus norvegicus (strain:Wistar) Adult Kidney cDNA to mRNA.
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REFERENCE  1 (sites)
AUTHORS   Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.
TITLE     Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
SCDGF/pdgf-C/fallotin
JOURNAL   Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
PUBMED    11162582
REFERENCE  2 (bases 1 to 1116)
AUTHORS   Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE     Direct Submission
JOURNAL   Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,
Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo
113-8602, Japan (E-mail:t-hamada@nms.ac.jp,
Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)
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LOCUS AB033829 1675 bp mRNA VRT 26-JUL-2000
DEFINITION Gallus gallus SCDGF mRNA for spinal cord-derived growth factor,
complete cds.
ACCESSION AB033829
VERSION AB033829.1 GI:9392291
KEYWORDS spinal cord-derived growth factor; scdgf gene.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (sites)
Hamada,T., Ui-Tei,K. and Miyata,Y.
A novel gene derived from developing spinal cords, SCDGF, is a
unique member of the PDGF/VEGF family(1)
FEBS Lett. 475 (2), 97-102 (2000)
20317014
2 (bases 1 to 1675)
Hamada,T., Ui-Tei,K. and Miyata,Y.
Direct Submission
Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases.
Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology;
1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan
(E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277),
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LOCUS AX027968 279 bp DNA PAT 16-SEP-2000
DEFINITION Sequence 36 from Patent WO0037641.
ACCESSION AX027968
VERSION AX027968.1 GI:10188782
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 279)
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE Vascular endothelial growth factor-x
JOURNAL Patent: WO 0037641-A 36 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
SRIDEVI NAIDU (US)

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DEFINITION Sequence 57 from Patent WO0037641.
ACCESSION AX027989
VERSION AX027989.1 GI:10188803
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 279)
AUTHORS
Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE
Vascular endothelial growth factor-x
JOURNAL
Patent: WO 0037641-A 57 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
SRIDEVI NAIDU (US)
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DEFINITION Sequence 36 from Patent WO0037641.
ACCESSION AX028065
VERSION AX028065.1 GI:10188874
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 279)
AUTHORS
Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE
Vascular endothelial growth factor-x
JOURNAL
Patent: WO 0037641-A 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
SRIDEVI NAIDU (US)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
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/note="Human EST"
BASE COUNT      86 a      60 c      66 g      67 t
ORIGIN

alignment_scores:
  Quality: 513.00      Length: 93
  Ratio: 5.516         Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

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38 uTyrSerCysThrProArgAsnPheSerValSerIleArgGluGluLeuL 55
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; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1325 base pairs
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; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2029 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
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; TISSUE TYPE: Human Lung
; US-08-915-795-4

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; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Evenson, McKown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-08-915-795-1

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  Percent Similarity: 50.658      Percent Identity: 28.289

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14 .....LeuGlyLysAlaPheValP 20
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1881 ATCAGGCTGAGGCTCAAAAGTTTTTACCAGTATGAGACTTCGCTCAGCAT 1930
20 heGlyArgLysSerArg.....ValValAspLeu 29
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1931 CCCATCGGTCCACTAGGTTTCGGGCACTTCTATGACATTGAAACACTA 1980
30 AsnLeuLeuThrGluValArgLeuTyrSerCysThrProArgAsnPh 46
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1981 AAAGTTATAGATGAAGATGCAAGAAGACTCAGTCGAGCCCTAGAGAAAC 2030
46 eSerValSerIleArgGluGluLeu...LysArgThrAspThrIlePheT 62
|||||:||||| ||| |||
2031 GTGCGTGGAGGTGGCCAGTACAGTGGGGAAGAGTACCAACACATCTTCA 2080
62 rpProGlyCysLeuValLysArgCysGlyGlyAsnCysAlaCysCys 78
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2081 AGCCCCCTTGTGTGAACGTGTTCCGATGTGTGGC.....TGTTCG 2121
79 LeuHisAsnCysAsnGluCys...GlnCysValProSerLysValThrLy 94
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2122 AATGAGAGAGCCCTTATCTGTATGAACACACCAGCCTCGTACATTCCAA 2171

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324 ATCGCTGAACACAGCTATGATCGCTGAATGTAAAGACTAGAACTAAGTTTTC 275

47 rValSerIleArgGluLeuLysArgThrAspThrIlePhe.....T 62
| | | : : : : : | | | | : : : : : | | |
274 GAAATCTCCAGAAGATTCGATCGACACAACTAACGCTAACTTCTTGTTT 225

62 rpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCys 78
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224 GGCCACCATTGTGTGAAGTTCAAAGATGTCTCGT.....TGTTCGT 184

79 LeuHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
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95 stYrHisGluValLeuGlnLeuArgPro.....LysThrGlyV 108
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108 al.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGlu 121
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113 TCGTTTAGAAGAAGCAATCTTCAAGAAGCTACT...GTACTTTGGAA 67

122 HisHisGluGluCysAspCys 128

66 GACCATTTCGGCTTCGTAAAGTGT 46
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seq_documentation_block:
  Sequence 4, Application US/09340250
  Patent No. 6083723
  GENERAL INFORMATION:
  APPLICANT: Tekamp-Olson, Patricia
  TITLE OF INVENTION: METHOD FOR EXP
  TITLE OF INVENTION: PROTEINS IN Y
  NUMBER OF SEQUENCES: 41
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Bell Seltzer IP Group
  STREET: 3605 Glenwood Ave. Sult
  CITY: Raleigh
  STATE: NC
  COUNTRY: US
  ZIP: 27622
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patent In Release #1.0.0
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/340,250
  FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/989,251
  FILING DATE:
  ATTORNEY/AGENT INFORMATION:
  NAME: Spruill, W. Murray
  REGISTRATION NUMBER: 32,943
  REFERENCE/DOCKET NUMBER: 5784-4
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 919 420 2202
  TELEFAX: 919 881 3175
  INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 352 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: other nucleic acid
  DESCRIPTION: /desc = "Complement
  DESCRIPTION: preceding SEQ ID N
  DESCRIPTION: produced upon asse
  ORIGINAL SOURCE:

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32 LeuThrGluGluValArgLeuTyrSerCysThrProArg...AsnPhcSe 47

مجلس، ۱۳۰۲


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alignment_scores:
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  Ratio: 1.528         Gaps: 12
  Percent Similarity: 51.429  Percent Identity: 32.857

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151 GAGCTGGAGAGCTTGGCTGCT.....CTGGTTCCCTGACCATTG 171
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
172 .....GGAAGAGGAGC.....CTGGTTCCCTGACCATTG 202
34 ..GluGluValArgLeuTyrSerCysThrProArgAsn.....PheSer 47
203 CTGAGCGGCCCATGATCGCGGAGTGCAGACGCGCACCGAGGTGTTGAG 252
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
253 ATCTCC...CGCGCCTCATAGACCGCACCAACGCCAACCTTCTGTGTTG 299
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79
300 GCGGCCCTGTGGAGTGCAGCGCTGCTCCGCG.....TGCTGC. 339
79 euHisAsnCysAsnGlnCysGlnCysValProSerLysValThrLysLys 95
340 .....AACAAACGCAACGTGAGTGCAGCGCGCCGCCACCCAGGTG. 375
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
376 .....CAGCTGCACCTGTCCAGGTGAGAAAGATCGAGAT 410
108 L.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
411 TGTGGGAGAGACCAATCTTAAGAGGCCACG...GTGACGCTGGAG 457
122 isHisGluGluCysAspCys 128
458 ACCACCTGGCATGCAAGTGT 477

seq_name: /cgn2_5/ptodata/1/ina/backfiles1.seq:5194596-14

seq_documentation_block:
; Patent No. 5194596
; APPLICANT: FISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN
; C.; MITCHELL, RICHARD L.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/450.883
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:14:
; LENGTH: 671
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alignment_scores:
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  Ratio: 1.528         Gaps: 12
  Percent Similarity: 51.429  Percent Identity: 32.857

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18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
235 .....GGAAGAGGAGC.....CTGGTTCCCTGACCATTG 265
34 ..GluGluValArgLeuTyrSerCysThrProArgAsn.....PheSer 47
266 CTGAGCGGCCCATGATCGCGGAGTGCAGACGCGCACCGAGGTGTTGAG 315
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
316 ATCTCC...CGCGCCTCATAGACCGCACCAACGCCAACCTTCTGTGTTG 362
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79
363 GCGGCCCTGTGGAGTGCAGCGCTGCTCCGCG.....TGCTGC. 402
79 euHisAsnCysAsnGlnCysGlnCysValProSerLysValThrLysLys 95
403 .....AACAAACGCAACGTGAGTGCAGCGCGCCGCCACCCAGGTG. 438
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
439 .....CAGCTGCACCTGTCCAGGTGAGAAAGATCGAGAT 473
108 L.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
474 TGTGGGAGAGACCAATCTTAAGAGGCCACG...GTGACGCTGGAG 520
122 isHisGluGluCysAspCys 128
521 ACCACCTGGCATGCAAGTGT 540

seq_name: /cgn2_5/ptodata/1/ina/backfiles1.seq:5219739-14

seq_documentation_block:
; Patent No. 5219739
; APPLICANT: FISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN
; C.; MITCHELL, RICHARD L.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BVGF120 AND
; BVGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
; VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVGF120 AND BVGF121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/559,041
; FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 450,883
; FILING DATE: 14-DEC-1989
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:14:
; LENGTH: 739
5219739-14

alignment_scores:
  Quality: 110.00      Length: 140
  Ratio: 1.528         Gaps: 12
  Percent Similarity: 51.429  Percent Identity: 32.857

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222 GAGCTGGAGAGCTTGGCTCGT..... 242
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
  |||:::|||||
243 .....GGAAGAGGAGC.....CTGGTTCCTGACCATG 273
34 ..GluGluValArgLeuTySerCysThrProArgAsn.....PheSer 47
  |||:::|||||
274 CTGAGCGGCATGATCGCGAGTCAAGAGCGCGCACCGAGGTGTCGAG 323
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
  ::|||:::|||||
324 ATCTCC...CGCGCCTCATAGACCGCACCAACGCAACTTCTCGTG 370
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79
  |||:::|||||
371 GCCGCCCTGTGTGAGGTGACGCGTCTCGGC.....TGCTGC. 410
79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
  |||:::|||||
411 .....AACACCGGAAGAGTGCAGTGCCTGCCGCCACCCAGGTG..... 446
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
  |||:::|||||
447 .....CAGCTGCAGCTGCGAGGTGAGAAAGATCGAGAT 481
108 1.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
  ::|||:::|||||
482 TGTGCGGAAGAGCAATCTTTAAGAGGCCACG...GTGAGCTGGAAG 528
122 isHisGluGluCysAspCys 128
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-387-845-3

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seq_documentation_block:
; Sequence 3, Application US/08387845
; Patent No. 5665567
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; TITLE OF INVENTION: bicistronic vector system in mammalian cells
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,845
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: pMW-2 (Weich et al., 1986)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..762
; OTHER INFORMATION: /product= "PDGF-B"
; OTHER INFORMATION: precursor sequence"
; OTHER INFORMATION: /note= "human PDGF-B gene from pGEM2-PDGF-B,
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; OTHER INFORMATION: flanked by 5'-EcoRI und 3'-HindIII
; OTHER INFORMATION: restriction cleavage sites"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 283..609
; OTHER INFORMATION: /product= "mature PDGF-B chain"
; PUBLICATION INFORMATION:
; AUTHORS: Weich, H. A.
; AUTHORS: Seibald, W.
; AUTHORS: Schairer, H. U.
; AUTHORS: Hoppe, U.
; JOURNAL: FEBS Lett.
; VOLUME: 198
; PAGES: 344-348
; DATE: 1986
US-08-387-845-3
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Quality:	110.00	Length:	140
Ratio:	1.528	Gaps:	12
Percent Similarity:	51.429	Percent Identity:	32.857

alignment_block:

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253 GAGCTGGAGAGCTTGGCTCGT..... 273
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
  |||:::|||||
274 .....GGAAGAGGAGC.....CTGGTTCCTGACCATG 304
34 ..GluGluValArgLeuTySerCysThrProArgAsn.....PheSer 47
  |||:::|||||
305 CTGAGCGGCATGATCGCGAGTCAAGAGCGCGCACCGAGGTGTCGAG 354
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
  ::|||:::|||||
355 ATCTCC...CGCGCCTCATAGACCGCACCAACGCAACTTCTCGTG 401
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79
  |||:::|||||
402 GCCGCCCTGTGTGAGGTGACGCGTCTCGGC.....TGCTGC. 441
79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
  |||:::|||||
442 .....AACACCGGAAGAGTGCAGTGCCTGCCGCCACCCAGGTG..... 477
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
  |||:::|||||
478 .....CAGCTGCAGCTGCGAGGTGAGAAAGATCGAGAT 512
108 1.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
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513 TGTGCGGAAGAGCAATCTTTAAGAGGCCACG...GTGAGCTGGAAG 559
122 isHisGluGluCysAspCys 128
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-778-275-3

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seq_documentation_block:
; Sequence 3, Application US/08778275
; Patent No. 5935819
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; TITLE OF INVENTION: bicistronic vector system in mammalian cells
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DATE: 1986
US-08-867-352-3

alignment_scores:
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Ratio: 1.528 Gaps: 12
Percent Similarity: 51.429 Percent Identity: 32.857

alignment_block:
US-09-457-066-2_COPY_210_345 x US-08-867-352-3 ..
Align seg 1/1 to: US-08-867-352-3 from: 1 to: 868

2 AspLeuGluAspLeuTyArgProThrTrpGlnLeuLeuGlyLysAlaPh 18
253 GAGCTGGAGAGCTTGGCTCGT.....CTGGGTTCCCTGACCATTTG 273
18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
274GGAAGAAGGAGC.....CTGGGTTCCCTGACCATTTG 304
34 ..GluGluValArgLeuTySerCysThrProArgAsn.....PheSer 47
305 CTGAGCGCGCATGATCCCGAGTGCAGACCGCGACCGAGGTGTTCGAG 354
48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
355 ATCTCC...CGGCGCTCATAGACCGCACCAACGCAACTTCCTGGTGTG 401
62 pProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysL 79
402 GCCGCCCTGTCTGGAGTGCAGCGCTGTCTCCGCG.....TGCTGC. 441
79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
442ACAACCGCAACGTGCAGTCCCGCCCGCCAGGTG..... 477
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
478CAGCTGGACCTTCCAGGTGAGAAAGATCGAGAT 512
108 1.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
513 TGTGCGGAAGAAGCAATCTTTAAGAACGCCACG...GTGACGCTGGAAG 559
122 isHisGluGluCysAspCys 128
560 ACCACCTGGCATGCAAGTGT 579

seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-989-251-28

seq_documentation_block:
Sequence 28, Application US/08989251
Patent No. 6017731

GENERAL INFORMATION:
APPLICANT: Tekamp-Olson, Patricia
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN YEAST
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,251
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spuill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5784-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic chimera"
ORIGINAL SOURCE:
ORGANISM: Homo sapiens/Saccharomyces cerevisiae
FEATURE:
NAME/KEY: CDS
LOCATION: 454..1179
FEATURE:
NAME/KEY: misc_feature
LOCATION: 454..519
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NAME/KEY: transit_peptide
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OTHER INFORMATION: /function= "mediates protein
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NAME/KEY: mat_peptide
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FEATURE:
NAME/KEY: transit_peptide
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OTHER INFORMATION: /product= "PDGF-B prepeptide"
OTHER INFORMATION: /standard_name= "PDGF-B presequence"
US-08-989-251-28

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Quality: 110.00 Length: 140
Ratio: 1.528 Gaps: 12
Percent Similarity: 51.429 Percent Identity: 32.857

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18 eValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThr.... 33
688GGAAGAAGGAGC.....CTGGGTTCCCTGACCATTTG 718
34 ..GluGluValArgLeuTySerCysThrProArgAsn.....PheSer 47
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48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62

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79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
856 .....AACAAACCGAACGTGAGTGGCGGCCACCCAGGTG..... 891
96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
892 .....CAGCTGGCAGCTGTCCAGGTGAGAAAGATCGAGAT 926
108 1.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
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seq_documentation_block:
; Sequence 28, Application US/09340250
; Patent No. 6083723
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,250
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,251
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5784-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic chimera"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens/Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 454..1179
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 454..519
; OTHER INFORMATION: /product= "PDGF-B prepeptide"
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Ratio: 1.528 Gaps: 12
Percent Similarity: 51.429 Percent Identity: 32.857

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688 .....GGAAGAGAGAGC.....CTGGGTTCCCTGACCATG 718

34 ..GluGluValArgLeuTyrSerCysThrProArgAsn.....PheSer 47
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48 ValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....Tr 62
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816 GCGCCCTGTGTGGAGTGCAGCGCTGCTCCGC.....TGCTGC. 855

79 euHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLys 95
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856 .....AACAAACCGAACGTGAGTGGCGGCCACCCAGGTG..... 891

96 TyrHisGluValLeuGlnLeuArgPro.....LysThrGlyVa 108
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892 .....CAGCTGGCAGCTGTCCAGGTGAGAAAGATCGAGAT 926

108 1.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluH 122
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927 TGTGCGGAAGAACCAATCTTTAAGAGGCCAGC...GTGAGCTGGAAG 973

122 isHisGluGluCysAspCys 128
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974 ACCACCTGGCATCAAGTGT 993
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OM of: US-09-457-066-2_COPY_210_345 to: N_Geneseq_0601.* out_format : pfs

Date: Aug 18, 2001 4:13 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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Search information block:

Query: US-09-457-066-2_COPY_210_345

Query length: 136

Database: N_Geneseq_0601.*

Database sequences: 730101

Database length: 313950809

Search time (sec): 113.960000

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seq_documentation_block:

ID AAA51540 standard; cDNA; 1095 BP.

AC AAA51540;

DT 26-SEP-2000 (first entry)

DE MBP-ZVEGF3 fusion protein coding sequence.

KW Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW Chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
KW vulnary; maltose binding protein; MBP; ss.

OS Chimeric - Homo sapiens.

OS Chimeric - Synthetic.

PN WO200034474-A2.

PD 15-JUN-2000.

PF 07-DEC-1999; 99WO-US28968.

PR 07-DEC-1999; 98US-0207120.

PR 06-JUL-1999; 99US-0142576.

PR 21-OCT-1999; 99US-0161653.

PR 12-NOV-1999; 99US-0165255.

PA (ZYMO) ZYMOGENETICS INC.

PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

PI Gilbertson DG, West JW;

XX WPI; 2000-423420/36.

XX Novel zvegf3 polypeptides and nucleotides encoding them useful for
stimulating growth of smooth muscle cells and fibroblasts comprising an
epitope bearing portion of a specific amino acid sequence

XX Example 28; Page 172-173; 173pp; English.

This DNA encodes human ZVEGF3 (a novel vascular endothelial growth
factor homologue) fused N-terminally to maltose binding protein (MBP).
Polypeptides comprising an epitope-bearing portion human or murine
ZVEGF3 are claimed. The growth factors comprise a growth factor domain
and a CUB domain (genetic sequence motifs are shown in AA96859 and
AA96860). The growth factor domain is characterized by an arrangement of
cysteine residues and beta-strands that is characteristic of the
"cysteine knot" structure of the platelet-derived growth factor (PDGF)
family. The CUB domain shows homology to CUB domains in neuropilins,
human bone morphogenetic protein-1, porcine seminal plasma protein,
bovine acidic seminal fluid protein and Xenopus laevis tolloid-like
protein. Structural analysis and homology predict that ZVEGF3
polypeptides complex with a second polypeptide to form multimeric
proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.

ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
muscle cells, for activating cell surface PDGF-alpha receptor and for
inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
useful for regulating (post-development) organ growth, regeneration and
maintenance, as well as tissue maintenance and repair processes. ZVEGF3
antagonists are useful for treating cancer, rheumatoid arthritis,
diabetic retinopathy, ischemic limb disease, peripheral vascular
disease, myocardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound
healing, chronic liver disease and hemangioma formation. ZVEGF3 can also

CC be used to modulate neurite growth and development of the nervous system,
CC and for treating neurodegenerative diseases.
XX
SQ Sequence 1095 BP; 320 A; 227 C; 267 G; 281 T; 0 other;

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Ratio: 5.544 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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717 TTTTCTTTTGGAGAAAATCCAGAGTGTGTGATCTGAACTTCTTAACAG 766
34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
|||||
767 AGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 816
51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
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917 AATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGTCTT 966
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
967 CAGTTGACCAACAAAGCCGGTGTAGGGGATTCACAAATCACTACCCA 1016
117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134
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134 hrGlyGly 136
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1067 CAGGAGGA 1074

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seq_documentation_block:

ID AAA71985 standard; DNA; 1096 BP.

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AC

XX

XX

DT 19-JAN-2001 (first entry)

XX

DE

XX

VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
angiogenesis regulator; vascularization regulator; cancer; psoriasis;
rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
venous sore; diabetic ulcer; burns; skin graft growth; ds.

OS Homo sapiens.

XX

XX

FH Key

Location/Qualifiers

FT CDS 3..1070
FT /*tag= a
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PN WO200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

XX

PR 18-MAR-1999; 99US-0124967.

XX

PR 08-NOV-1999; 99US-0164131.

XX

PA (JANC) JANSSEN PHARM NV.

XX

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

XX

XX P-PSDB; AAB10641.

PT New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

XX

XX such as cancer, rheumatoid arthritis, psoriasis and wounds -

PS Disclosure; Fig 21; 127pp; English.

XX

XX This invention describes a novel vascular endothelial growth factor-X

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and

CC antidiabetic activity and acts as an angiogenesis and vascularization

CC regulator. An antisense molecule of the invention is useful for treating

CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate

CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ

CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote

CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or

CC vascularization. This sequence encodes a human VEGF-X protein which can

CC be expressed in E. coli systems and which is described in the method of

XX the invention.

XX

SQ Sequence 1096 BP; 337 A; 225 C; 253 G; 281 T; 0 other;

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Quality: 754.00 Length: 136
Ratio: 5.544 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
|||||
692 TTTTCTTTTGGAGAAAATCCAGAGTGTGTGATCTGAACTTCTTAACAG 741
34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
|||||
742 AGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 791
51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
|||||

XX DE Human VEGF-X DNA for expression in Baculovirus/insect cell systems.
 XX KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytotstatic;
 XX KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 XX venous sore; diabetic ulcer; burns; skin graft growth; ds.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 63..1127
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 XX WO200037641-A2.
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 XX 29-JUN-2000.
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 XX 21-DEC-1999; 99WO-US30503.
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 XX 22-DEC-1998; 98GB-0028377.
 XX 18-MAR-1999; 99US-0124967.
 XX 08-NOV-1999; 99US-0164131.
 XX
 XX (JANC) JANSSEN PHARM NV.
 XX
 XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
 XX Dhanaraj SN, Xu J;
 XX WPI; 2000-442669/38.
 XX P-PSDB; AAB10640.
 XX
 XX New vascular endothelial growth factor protein, useful for treating or
 XX preventing diseases associated with inappropriate angiogenesis activity
 XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
 XX
 XX Disclosure; Fig 20; 127pp; English.
 XX
 XX This invention describes a novel vascular endothelial growth factor-X
 XX (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
 XX vulnerary, cytotstatic, antirheumatic, antiarthritic, antipsoriatic and
 XX antidiabetic activity and acts as an angiogenesis and vascularization
 XX regulator. An antisense molecule of the invention is useful for treating
 XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 XX retinopathy by inhibiting angiogenic activity or inappropriate
 XX vascularization including formation and proliferation of new blood
 XX vessels, growth and development of tissues, tissue regeneration and organ
 XX and tissue repair in a subject. The products of the invention are useful
 XX for preparing medicaments for treating wounds such as dermal ulcers,
 XX pressure sores, venous sores, diabetic ulcers and burns and to promote
 XX skin graft growth, tissue repair, proliferation of new blood vessels,
 XX tissue regeneration and organ repair by promoting angiogenic activity or
 XX vascularization. This sequence encodes a human VEGF-X protein which can
 XX be expressed in Baculovirus/insect cell systems and which is described in
 XX the method of the invention.
 XX
 XX Sequence 1134 BP; 339 A; 225 C; 254 G; 316 T; 0 other;

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 Percent Similarity: 100.000 Percent Identity: 100.000

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 17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
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 767 TTTGTTTTTGAAGAAATCCAGAGTGGTGATCTGAACCTTCTAACAG 816
 |||||||
 34 luGluValArgLeuTyrSerCysThrProArgAsnPheserValserlle 50
 |||||||
 817 AGGAGGTAAGATTATACAGCTCCACACCTCGTAACCTTCTCAGTGTCCATA 866
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 51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
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 917 GGTAAACGCTGTGGTGGAACTGTGCCTGTGTCTCCACAATTCGCAATG 966
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 1017 CAGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCACCGA 1066
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 AC AAA71955;
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 XX DT 19-JAN-2001 (first entry)
 XX
 XX DE Human VEGF-X DNA isolated from clones 4 and 7.
 XX
 KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytotstatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 XX venous sore; diabetic ulcer; burns; skin graft growth; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200037641-A2.
 XX
 XX 29-JUN-2000.
 XX
 XX 21-DEC-1999; 99WO-US30503.
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 XX 22-DEC-1998; 98GB-0028377.
 XX 18-MAR-1999; 99US-0124967.
 XX 08-NOV-1999; 99US-0164131.
 XX
 XX (JANC) JANSSEN PHARM NV.
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 XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
 XX Dhanaraj SN, Xu J;
 XX WPI; 2000-442669/38.
 XX P-PSDB; AAB10635, AAB10636.

PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT Such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Claim 4; Fig 9; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (1a) and its encoding polynucleotide (11a) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence encodes the human VEGF-X protein isolated
CC from clones 4 and 7 described in the method of the invention.
XX
SQ Sequence 1473 BP; 406 A; 321 C; 361 G; 385 T; 0 other;

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Quality: 754.00 Length: 136
Ratio: 5.544 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
884 TTGGACTTAGAAGACTATATAGGCCAACTTGGCAACTTCTTGGCAAGGC 933
17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuThrG 34
TTTTTTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAACAG 983
34 LuGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
AGGAGGTAAGATTATACAGTCCACACCTCGTAACCTCTCAGTGCCTA 1033
51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
AGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTGTCTCT 1083
67 uValLysArgCysGlyGlyAspCysAlaCysCysLeuHisAsnCysAsnG 84
GGTAAACCGTGTGGGAACTGTGCCTGTGTCTCCAAATGCAATG 1133
84 LuCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
AATGTCATGTGTCCCAAGCAAGTTACTAAAAATACCAACAGGTCCTT 1183
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
CAGTTGAGACCAAAACACCGGTGTCAGGGCATTCACAAATCACTACCCA 1233
117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134
CGTGCCCTTGAGCACCATTAGGAGTGTGACTGTGTGTGCAGAGGAGCA 1283
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1284 CAGGAGGA 1291

seq_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT: AAC81582

seq_documentation_block:
ID AAC81582 standard; DNA; 1760 BP.
XX
AC AAC81582;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human zveg3 DNA, SEQ ID NO:32.
XX
KW Human; zveg3; zveg3 fusion; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
KW immunomodulation; hepatic; ds.
OS Homo sapiens.
XX
PN WO2000066736-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US40047.
XX
PR 03-MAY-1999; 9905-0304216.
PR 10-NOV-1999; 9905-0164463.
PR 04-FEB-2000; 2000US-0180169.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
DR WPI: 2000-687541/67.
DR P-PSDB; AAB48657.
XX
PT Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
PS Claim 25; Page 123-125; 143pp; English.
XX
CC The invention relates to the human growth factor homologue zveg3
CC (AAB48653), and nucleic acids encoding it (AAC81555). zveg3 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. zveg3 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. zveg3 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zveg3 or fragments thereof, particularly human zveg3/human zveg3
CC fusions; expression constructs and host cells comprising human zveg3
CC nucleic acids; the recombinant expression of human zveg3; an antibody
CC which binds to human zveg3 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg3-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zveg3-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zveg3 gene of a patient. zveg3 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may also be
CC used in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents DNA encoding human
CC zveg3.
XX

Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;

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  Ratio: 5.544         Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
831 TTTTGTGTTTTGGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 880

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
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51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67
931 AGGGAAGAACTAAAGAGAACCCGATACCATTTCTGGCCAGGTTGTCCT 980

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
981 GGTAAACGCTGTGGGGAACTGTGCTGTGTCTCCAAATGCAATGCAATG 1030

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
1031 AATGTCAATGTGTCCCAAGCAAGTACTTAAATAATACCAGAGTCTCT 1080

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
1081 CAGTTAGACCAAGAACCGGTGTGCAGGGGATTCACAAATCACTCACCGA 1130

117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134
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134 hrCglyGly 136
1181 CAGGAGGA 1188

seq_name: /SIDS8/cgdata/geneseq/geneseq/NA2000.DAT:AAA51498
seq_documentation_block:
ID AAA51498 standard; cDNA; 1760 BP.
XX
AC AAA51498;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human growth factor homologue, ZVEGF3, cDNA.
XX
KW Vascular endothelial growth factor; homologue; zvegfg3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
KW vulnary; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 154..1191
FT FT /*tag= a
FT FT /product= ZVEGF3
FT FT 154..195
FT FT /*tag= b
FT
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XX WO200034474-A2.
XX
XX 15-JUN-2000.
XX
XX 07-DEC-1999; 99WO-US28968.
XX
XX 07-DEC-1998; 98US-0207120.
XX 06-JUL-1999; 99US-0142576.
XX 21-OCT-1999; 99US-0161653.
XX 12-NOV-1999; 99US-0165255.
XX
XX (Zymo ) ZYMOGENETICS INC.
XX
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
XX Gilbertson DG, West JW;
XX
XX WPI; 2000-423420/36.
XX P-PSDB; AAY96858.
XX
XX Novel zvegfg3 polypeptides and nucleotides encoding them useful for
XX stimulating growth of smooth muscle cells and fibroblasts comprising an
XX epitope bearing portion of a specific amino acid sequence
XX
XX Claim 29; Page 146-148; 173pp; English.
XX
XX This cDNA encodes a human vascular endothelial growth factor homologue,
XX designated ZVEGF3. Polypeptides comprising an epitope-bearing portion
XX human or murine ZVEGF3 are claimed. The growth factors comprise a growth
XX factor domain and a CUB domain (generic sequence motifs are shown in
XX AAY96859 and AAY96860). The growth factor domain is characterized by an
XX arrangement of cysteine residues and beta-strands that is characteristic
XX of the "cysteine knot" structure of the platelet-derived growth factor
XX (PDGF) family. The CUB domain shows homology to CUB domains in
XX neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
XX protein, bovine acidic seminal fluid protein and Xenopus laevis
XX toll-like protein. Structural analysis and homology predict that
XX ZVEGF3 polypeptides complex with a second polypeptide to form multimeric
XX proteins. The human zvegfg3 gene has been mapped to chromosome 4q28.3.
XX ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
XX muscles cells, for activating cell surface PDGF-alpha receptor and for
XX inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
XX useful for regulating (post-development) organ growth, regeneration and
XX maintenance, as well as tissue maintenance and repair processes. ZVEGF3
XX antagonists are useful for treating cancer, rheumatoid arthritis,
XX diabetic retinopathy, ischemic limb disease, peripheral vascular
XX disease, myocardial ischemia, vascular intimal hyperplasia,
XX atherosclerosis, wound healing, chronic liver disease and haemangioma
XX formation. ZVEGF3 can also be used to modulate neurite growth and
XX development of the nervous system, and for treating neurodegenerative
XX diseases.
XX
XX Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;
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alignment_scores:
  Quality: 754.00      Length: 136
  Ratio: 5.544         Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_210_345 x AAA51498
Align seg 1/1 to: AAA51498 from: 1 to: 1760
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1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
781 TTGGACTTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGCAAGGC 830

17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
831 TTTTGTGTTTTGGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 880
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34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
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 881 AGGAGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 930
 |||||
 51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
 |||||
 931 AGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTCCT 980
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 67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
 |||||
 981 GGTAAACGCTGTGTGGCAACTGTCCCTGTGTCTCCACAATTTGCAATG 1030
 |||||
 84 luCysGlnCysValProSerLysValThrLysLysThrHisGluValLeu 100
 |||||
 1031 AATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCCAGGAGTCTT 1080
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 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
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 117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySert 134
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 1131 CGTGGCCCTGGAGCACCATCAGGAGTGTGACGTGTGTGTGCAGAGGAGCA 1180
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 1181 CAGGAGGA 1188
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seq_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA12523

seq_documentation_block:

ID AAA12523 standard; cDNA; 2108 BP.

AC AAA12523;

XX 25-JUL-2000 (first entry)

XX cDNA encoding platelet-derived growth factor C (PDGF-C).

XX platelet-derived growth factor C; PDGF-C; cell proliferation;
 KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
 KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
 KW chorlocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
 XX lung carcinoma; erythroleukemia; tissue remodelling; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 37..1073

FT /*tag= a

FT /product= "platelet-derived growth factor C"

XX WQ200018212-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US22668.

XX 30-SEP-1998; 98US-0102461.

XX 12-NOV-1998; 98US-0108109.

XX 03-DEC-1998; 98US-0110749.

XX 18-DEC-1998; 98US-0113002.

XX 21-MAY-1999; 99US-0135426.

XX 15-JUL-1999; 99US-0144022.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD.

XX Eriksson U, Aase K, Lee X, Ponten A, Untela M, Alitalo K;

PI Oestman A, Heldin C, Betsholz C;

XX WPI; 2000-252954/25.

DR P-PSDB; AAY84557.

DR

XX
 PT
 PT

Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C receptor

Claim 9; Fig 1; 135pp; English.

XX

The present sequence encodes human platelet-derived growth factor C (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor.

XX

PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The

XX

PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C. PDGF-C can also be used to promote fibroblast

XX

mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour

XX

expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma

XX

and erythroleukemia, can be identified by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue

XX

remodelling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions, especially found in the lung, kidney or liver.

XX

SQ Sequence 2108 BP; 623 A; 400 C; 451 G; 629 T; 5 other;

alignment_scores:

Quality: 754.00

Ratio: 5.544

Percent Similarity: 100.000

Length: 136

Gaps: 0

Percent Identity: 100.000

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Align seg 1/1 to: AAA12523 from: 1 to: 2108

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|||||

664 TTGACCTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGC 713

|||||

17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuThrG 34

|||||

714 TTTTGTGTTTGGAGAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 763

|||||

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

|||||

764 AGGAGTTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 813

|||||

51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67

|||||

814 AGGAGAGAACTAAAGAGAACCGATACCATTTCTGCGCAGGTTGTCTCCT 863

|||||

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

|||||

864 GGTAAACGCTGTGTGGGAACCTGTGCTGTGTCTCCACAATTTGCAATG 913

|||||

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

|||||

914 AATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCCAGGAGTCTT 963

|||||

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117

|||||

964 CAGTTGAGACCAAGACCGGTGTGAGGGATTGCACAATCATCTACCGA 1013

|||||

117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySert 134

|||||

1014 CGTGGCCCTGGAGCACCATCAGGAGTGTGACTGTGTGTGCAGAGGAGCA 1063

|||||

134 hrGlyGly 136
|||||
1064 CAGGAGGA 1071

seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71951

seq_documentation_block:
ID AAA71951 standard; DNA; 2475 BP.

XX AC AAA71951;

XX DT 19-JAN-2001 (first entry)

XX DE Human RACE generated VEGF-X DNA.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 122..1159

XX FT /*tag= a

XX FT /product= "VEGF-X"

XX PN WO200037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC) JANSSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX DR P-PSDB; AAB10633.

XX PT New vascular endothelial growth factor protein, useful for treating or
preventing diseases associated with inappropriate angiogenesis activity
such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX PS Disclosure; Fig 6; 127pp; English.

XX CC This invention describes a novel vascular endothelial growth factor-X
(VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
antidiabetic activity and acts as an angiogenesis and vascularization
regulator. An antisense molecule of the invention is useful for treating
or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
retinopathy by inhibiting angiogenic activity or inappropriate
vascularization including formation and proliferation of new blood
vessels, growth and development of tissues, tissue regeneration and organ
and tissue repair in a subject. The products of the invention are useful
for preparing medicaments for treating wounds such as dermal ulcers,
pressure sores, venous sores, diabetic ulcers and burns and to promote
skin graft growth, tissue repair, proliferation of new blood vessels,
tissue regeneration and organ repair by promoting angiogenic activity or
vascularization. This sequence encodes the RACE generated human VEGF-X
protein described in the method of the invention.

XX SQ Sequence 2475 BP; 730 A; 473 C; 523 G; 749 T; 0 other;

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Quality: 754.00 Length: 136
Ratio: 5.544 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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34 luGluValArgLeuTyrSerCysThrProArgAsnPheserValSerlle 50
|||||
849 AGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 898

51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeule 67
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899 AGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTGTCTCT 948

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
|||||
949 GGTAAACGCTGTGGTGGGAACTGTGCCTGTGTCTCCACAATTCGAATG 998

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValleu 100
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999 AATGTCAATGTCTCCAAAGAAAGTTACTAAAAAATACCACGAGGTCTT 1048

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
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1049 CAGTTGAGACCAAGACCGGTGTACGGGATTCACAAATCACTCACCGA 1098

117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134
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1099 CGTGGCCCTGGAGCACCATGAGGAGTGTGACGTGTGTGTGCAGAGGGAGCA 1148

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seq_documentation_block:

ID AAA71990 standard; cDNA; 2668 BP.

XX AC AAA71990;

XX DT 19-JAN-2001 (first entry)

XX DE Human VEGF-X cDNA.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 267..1304

XX FT /*tag= a

XX FT /product= "VEGF-X"

XX PN WO200037641-A2.

PD 29-JUN-2000.
XX
PF
XX 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
XX (JANC) JANSSEN PHARM NV.
XX
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
XX WPI: 2000-442669/38.
DR P-PSDB; AAB10644.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 30B; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence encodes a human VEGF-X protein described
XX in the method of the invention.
XX
SQ Sequence 2668 BP; 780 A; 511 C; 567 G; 810 T; 0 other;

alignment_scores:
Quality: 754.00 Length: 136
Ratio: 5.544 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_210_345 x AAA71990 ..
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17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
|||||
944 TTTTGTCTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAG 993
34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
|||||
994 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATA 1043
51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
|||||
1044 AGGGAAGAACTTAAAGAGAACCGATACCATTTTCTGGCCAGGTGTCTCT 1093
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
|||||
1094 GGTAAACCGCTGTGGTGGAACTGTGCTGTCTCCAAATTCGAATG 1143
84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

|||||
1144 AATGTCATGTGTCCTCCCAAGCAAGTTACTTAAAAATACCACGAGTCTT 1193
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
1194 CAGTTGAGACCAAGACCGGTGTCTCAGGGGATTGCACAAATCACTCACCGA 1243
117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134
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1244 CGTGGCCCTGGAGCACCATCAGGAGTGTGACTGTGTGTGCAGAGGAGCA 1293
134 hrGlyGly 136
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1294 CAGGAGGA 1301

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seq_documentation_block:
ID AAA71952 standard; DNA; 2776 BP.
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XX AC AAA71952;
XX
XX DT 19-JAN-2001 (first entry)
XX
XX DE Human VEGF-X homologue DNA.
XX
XX KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 260..1297
FT /*tag= a
FT /product= "VEGF-X homologue"
XX
XX PN WO200037641-A2.
XX
XX PD 29-JUN-2000.
XX
XX PF 21-DEC-1999; 99WO-US30503.
XX
XX PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
XX PA (JANC) JANSSEN PHARM NV.
XX
XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
XX DR WPI: 2000-442669/38.
DR P-PSDB; AAB10634.
XX
XX PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX PS Disclosure; Fig 7; 127pp; English.
XX
XX CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ

CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence encodes the human VEGF-X protein homologue
 CC described in the method of the invention.

XX SQ Sequence 2776 BP; 825 A; 515 C; 587 G; 849 T; 0 other;

alignment_scores:
 Quality: 754.00 Length: 136
 Ratio: 5.544 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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 17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
 937 TTTTGTGTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAG 986
 34 luCluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50
 987 AGGAGTAAAGATTATACAGTCGACACCTCGTAACCTTCTCAGTGTCCATA 1036
 51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67
 1037 AGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTGTCCTCT 1086
 67 uValLysArgCysGlyCysAsnCysAlaCysCysLeuHisAsnCysAsnG 84
 1087 GGTAAACGCTGGTGGGAACCTGCTGCTGCTCCACAATTTGCAATG 1136
 84 lucysGlnCysValProSerLysValThrLysLysThrHisGluValLeu 100
 1137 AATGTCATGTCGTCACCAAGAAATGTTACTAAAAAATACACAGAGTCTT 1186
 101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
 1187 CAGTTGAGACCAAGACCGGTGTCAGGGGATTCACAAATCACTCACCGA 1236
 117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySerT 134
 1237 CGTGGCCCTGGAGCACCACATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 1286
 134 hrGlyGly 136
 1287 CAGGAGGA 1294

seq_name: /SID58/gcgdata/geneseq/geneseq/NA2000.DAT:AAA52458

seq_documentation_block:

ID AAA52458 standard; cDNA; 2779 BP.

XX AC

XX AC

XX AC

XX 25-SEP-2000 (first entry)

XX cDNA encoding human growth factor related molecule GFRP-4.

XX DE

XX Human GFRP-4; growth factor related molecule; diseased breast tissue;
 KW bone morphogenetic protein 1; BMP-1; inflammation; immune response;
 KW reproductive tissue; reproductive tissue; developmental disorder; cell
 KW proliferative disorder; immune disorder; reproductive disorder;
 KW cardiovascular disorder; bacterial infection; viral; fungal; parasitic;

KW cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis; consensus;
 KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 258..1295

FT /*tag= a

FT /product= "Human GFRP-4"

XX WO200024774-A2.

XX PD 04-MAY-2000.

XX PF 28-OCT-1999; 99WO-US25458.

XX PR 28-OCT-1998; 98US-0181711.

XX PR 11-DEC-1998; 98US-0209547.

XX PR 17-MAY-1999; 99US-0313457.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Tang YT, Yue H, Hillman JL, Corley NC, Guegler KJ, Baughn MR;

XX PI Au-Young J;

XX WPI; 2000-350695/30.

XX DR P-PSDB; AAB03003.

XX PT Human growth factor related molecule protein useful for the diagnosis

XX PT and treatment of disorders associated with its activity including

XX PT developmental, cell proliferative, immune, reproductive and

XX PT cardiovascular disorders and infections -

XX PS Claim 9; Page 76; 80pp; English.

XX CC This sequence represents cDNA encoding human growth factor related

XX CC molecule GFRP-4. cDNA encoding GFRP-4 was initially identified in a

XX CC diseased breast tissue cDNA library, and the present sequence represents

XX CC a consensus derived from several overlapping and/or extended cDNA

XX CC clones. GFRP-4 has chemical and structural homology with human bone

XX CC morphogenetic protein 1 (BMP-1) (27% identity at the BMP-1 C-terminus).

XX CC GFRP-4 was found by Northern analysis to be expressed in reproductive

XX CC and cardiovascular tissue, and in cDNA libraries associated with cancer,

XX CC inflammation and the immune response. GFRP proteins (AAB03000-B03003),

XX CC nucleotides encoding them (AAA52455-A52458), GFRP agonists and

XX CC antagonists may be used to treat a wide variety of diseases associated

XX CC with increased or decreased expression or activity of GFRP proteins.

XX CC Conditions which may be treated include developmental disorders, cell

XX CC proliferative disorders (e.g., cancers), immune disorders (e.g.,

XX CC allergies, asthma), reproductive disorders (e.g., menstrual cycle

XX CC disorders) cardiovascular disorders (e.g., arteriosclerosis) and

XX CC bacterial, viral, fungal or parasitic infections. Additionally, GFRP

XX CC proteins and nucleotides can be used in the diagnosis of such disorders.

XX SQ Sequence 2779 BP; 832 A; 515 C; 585 G; 847 T; 0 other;

alignment_scores:

Quality: 754.00 Length: 136

Ratio: 5.544 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_210_345 x AAA52458

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885 TTGGACTTAGAAGATCTATATAGCCCACTTGGCACTTCTTGGCAAGGC 934

17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34

935 TTTTGTGTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACAG 984
34 luCluValargLeuTySerCysThrProArgAsnPheserValSerIle 50
|||||
985 AGGAGTAAGATATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 1034
51 ArqGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
|||||
1035 AGGGAAGAACTAAAGAACCGATACCATTTCTGGCCAGGTTCTCTCCT 1084
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
|||||
1085 GGTAAACGCTGTGTGGGAACCTGTGCTGTCTCCACAATTCGAATG 1134
84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
|||||
1135 AATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGTCTT 1184
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
1185 CAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCCTCACCGA 1234
117 pValAlaLeuGluHisHisGluLuCysAspCysValCysArgGlySert 134
|||||
1235 CGTGGCCCTGGACACCATGAGAGTGTGACTGTGTGTCGAGAGGGAGCA 1284
134 hrGlyGly 136
|||||
1285 CAGGAGGA 1292

seq_name: /SID58/gcgdata/geneseq/geneseqn/NA1999.DAT.AAZ23691

seq_documentation_block:

ID_AAZ23691 standard; DNA; 2825 BP.

AC_AAZ23691;

DT 11-JAN-2000 (first entry)

DE Human VEGF-E DNA.

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KW treatment; cardiovascular disorder; endothelial disorder; therapy;
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KW angiogenic disorder; age-related macular degeneration; vascular disease;
KW neovascularization; tumor; gene mapping; ss.
XX

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 259..1296
FT /*tag= a
ET /product= "VEGF-E"

XX WO9947677-A2.

PN 23-SEP-1999.

XX 10-MAR-1999; 99WO-US05190.

XX 17-MAR-1998; 98US-0040220.

XX 02-NOV-1998; 98US-0184216.

XX (GETH) GENENTECH INC.

XX Ferrara N, Kuo SS;

XX WPI; 1999-580306/49.

XX P-PSDB; AAY33679.

XX New growth factor polypeptide useful for treating cardiovascular or
PT endothelial disorders, e.g. cardiac hypertrophy
XX

PS Claim 2; Fig 1; 122pp; English.

XX This invention describes the isolation of a novel human vascular
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
CC tranquillizer, vulnery and cardiant activity. VEGF-E can be administered
CC therapeutically, especially by expressing encoding polynucleotides, to
CC treat cardiovascular or endothelial disorders in mammals, especially
CC humans. It is useful in wound repair and tissue generation and
CC regeneration, and may especially be used to treat cardiac hypertrophy
CC It can be combined with a carrier in pharmaceutical compositions, which
CC can be administered to treat disorders as above. VEGF-E can be used to
CC screen for antagonists and agonists, and the antagonists administered to
CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
CC age-related macular degeneration. It can be used to generate antibodies,
CC useful therapeutically as antagonists, as above. The antibodies are also
CC useful to detect VEGF-E polypeptide, especially to diagnose
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
CC vascular disease, or neovascularization associated with tumor formation),
CC by contacting the antibody with a tissue sample and detecting formation
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
CC tissue samples. They can also be used to diagnose a disease or
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
CC sample. They may also be used to produce probes useful to detect related
CC sequences or for gene mapping. This sequence encodes the human VEGF-E
CC protein described in the method of the invention.

XX Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;

alignment_scores:

Quality: 754.00 Length: 136

Ratio: 5.544 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_210_345 x AAZ23691

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886.TTGGACTTAGAAGATCTATATAGGCCAACTTGCAACTTCTGGCAAGGC 935
17 aPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
936 TTTTGTGTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACAG 985
34 luCluValargLeuTySerCysThrProArgAsnPheserValSerIle 50
|||||
986 AGGAGTAAGATATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 1035
51 ArqGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
|||||
1036 AGGGAAGAACTAAAGAACCGATACCATTTCTGGCCAGGTTCTCTCCT 1085
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
|||||
1086 GGTAAACGCTGTGTGGGAACCTGTGCTGTCTCCACAATTCGAATG 1135
84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
|||||
1136 AATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGTCTT 1185
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
|||||
1186 CAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCCTCACCGA 1235
117 pValAlaLeuGluHisHisGluLuCysAspCysValCysArgGlySert 134
|||||

1236 CGTGGCCCTGGAGCACCATTGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 1285

134 hrGlyGly 136

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1286 CAGGAGGA 1293

seq_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA47452

seq_documentation_block:

ID AAA47452 standard; cDNA; 2839 BP.

XX

XX

AC AAA47452;

XX

DT 20-OCT-2000 (first entry)

XX

DE Human TANGO 128 coding sequence.

XX

KW TANGO: 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;

KW graft versus-host diseases; rheumatoid arthritis; psoriasis;

KW inflammatory bowel disease; septic shock; ulcerative colitis;

KW Crohn's disease; chronic myelogenous leukemia; cancer; liver

KW disease; Hodgkin's disease; osteoarthritis; Lyme's disease;

KW cachexia; autoimmune disease; myasthenia gravis; autoimmune diabetes;

KW systemic lupus erythematosus; transgenic animal; diagnosis;

KW prognosis; prophylactic; therapeutic; human; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 288..1325

FT /*tag= a

FT /product= TANGO 128

FT

PN WO200039284-A1.

XX

PN

XX

XX

PD 06-JUL-2000.

XX

XX

PF 23-DEC-1999; 99WO-US31025.

XX

XX

PR 30-DEC-1998; 98US-02233546.

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PA (MILL-) MILLENNIUM PHARM INC.

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PI Holtzman DA;

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alignment_scores:

Quality: 754.00

Ratio: 5.544

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_210_345 x AAA47452

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|||||||

915 TTGGACTTAGAAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAGGC 964

|||||||

17 aPheValPheGlySerArgValValAspLeuAsnLeuLeuThrG 34

|||||||

965 TTTTGTGTTTGGGAAGAAATCCAGAGTGGTGAACCTTCTTAACAG 1014

|||||||

34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 50

|||||||

1015 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGCATA 1064

|||||||

51 ArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeuLe 67

|||||||

1065 AGGCAAGAAGCTAAAGAGAACCGATACCATTTTCTGGCAGGTTGTCTCCT 1114

|||||||

67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84

|||||||

1115 GGTAAACGGTGTGGTGGAACTGTGCTGTGTCTCCACAATTCGAATG 1164

|||||||

84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100

|||||||

1165 AATGTCATGTGTCCCAAGCAAGTTACTAAAAAATACCAGAGGTCCTT 1214

|||||||

101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117

|||||||

1215 CAGTTGAGACCAAGACCGGTGTTCAGGGGATTGCACAAATCACTCACCGA 1264

|||||||

117 pValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerT 134

|||||||

1265 CGTGGCCCTGGAGCACCATTGAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 1314

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134 hrGlyGly 136

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1315 CAGGAGGA 1322

seq_name: /SIDS8/gcgdata/geneseq/geneseq/NA1999.DAT:AA234296

seq_documentation_block:

ID AA234296 standard; cDNA; 2849 BP.

XX

XX

AC AA234296;

XX

DT 07-DEC-1999 (first entry)

XX

XX

DE Human PRO200 nucleotide sequence.

XX

XX

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;

KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;

KW secreted protein; transmembrane protein; ss.

XX

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OS Homo sapiens.

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PN WO9946281-A2.

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PD 16-SEP-1999.

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PF 08-MAR-1999; 99WO-US05028.

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PR 10-MAR-1998; 98US-0077450.

PR

PR 11-MAR-1998; 98US-0077632.

PR

PR 11-MAR-1998; 98US-0077641.

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PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.

PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX (GETH ) GENENTECH INC.
PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
DR P-PSDB; AAY41766.
XX
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX
XX Claim 2; Fig 206; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

alignment_scores:
    Quality: 754.00      Length: 136
    Ratio: 5.544        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_210_345 x AA234296 ..
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. 1 LeuAspLeuGluAspLeuTyrArgProThrTrpGlnLeuLeuGlyLysAl 17
912 TTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTGGCAAGGC 961
17 apheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 34
962 TTTTGTGTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAACAG 1011
34 luGluValArgLeuTyrSerCysThrProArgAsnPheSerValserIle 50
1012 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATA 1061
51 ArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 67
1062 AGGGAAGAACTAAAGAACACCATTTCTTGGCCAGGTGTCTCTCT 1111
67 uValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnG 84
1112 GGTAAACGCTGTGGGGAACTGTGCTGTGTGTCTTCCAAATGCAATG 1161
84 luCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 100
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1162 AATGTCAATGTGTCCCAAGCAAGTTTACTAAAAAATACCACGAGGTCCTT 1211
101 GlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 117
1212 CAGTTGAGACCAAGACCGGTGTTCAGGGGATTGCACAAATCACTCACCGA 1261
117 pValAlaLeuGluHisGluGluCysAspCysValCysArgGlySert 134
1262 CGTGGCCCTGGAGCACCATCAGGAGTGTGACTGTGTGTGCAGAGGGAGCA 1311
134 hrGlyGly 136
1312 CAGGAGGA 1319